

FIG. 1

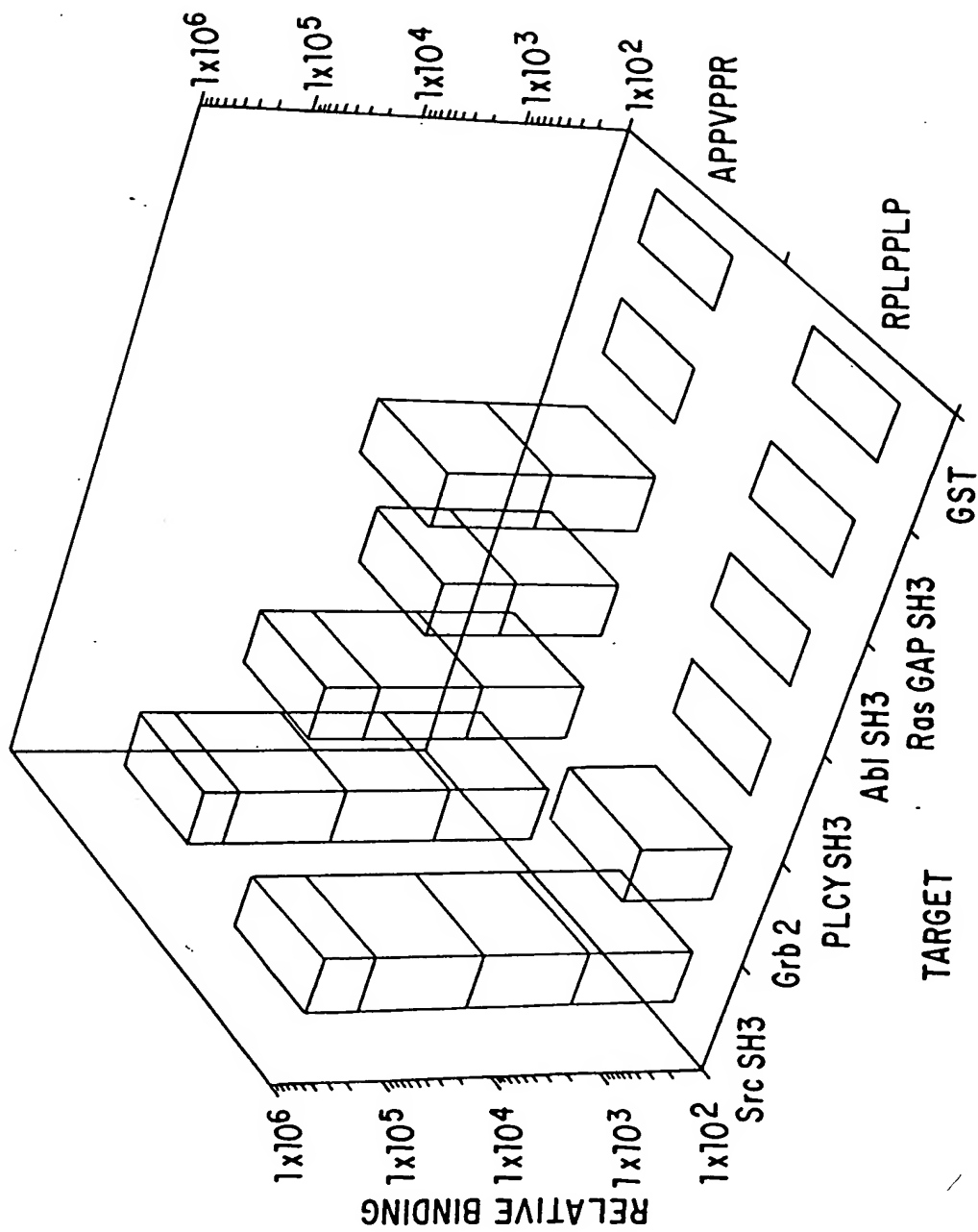


FIG. 2

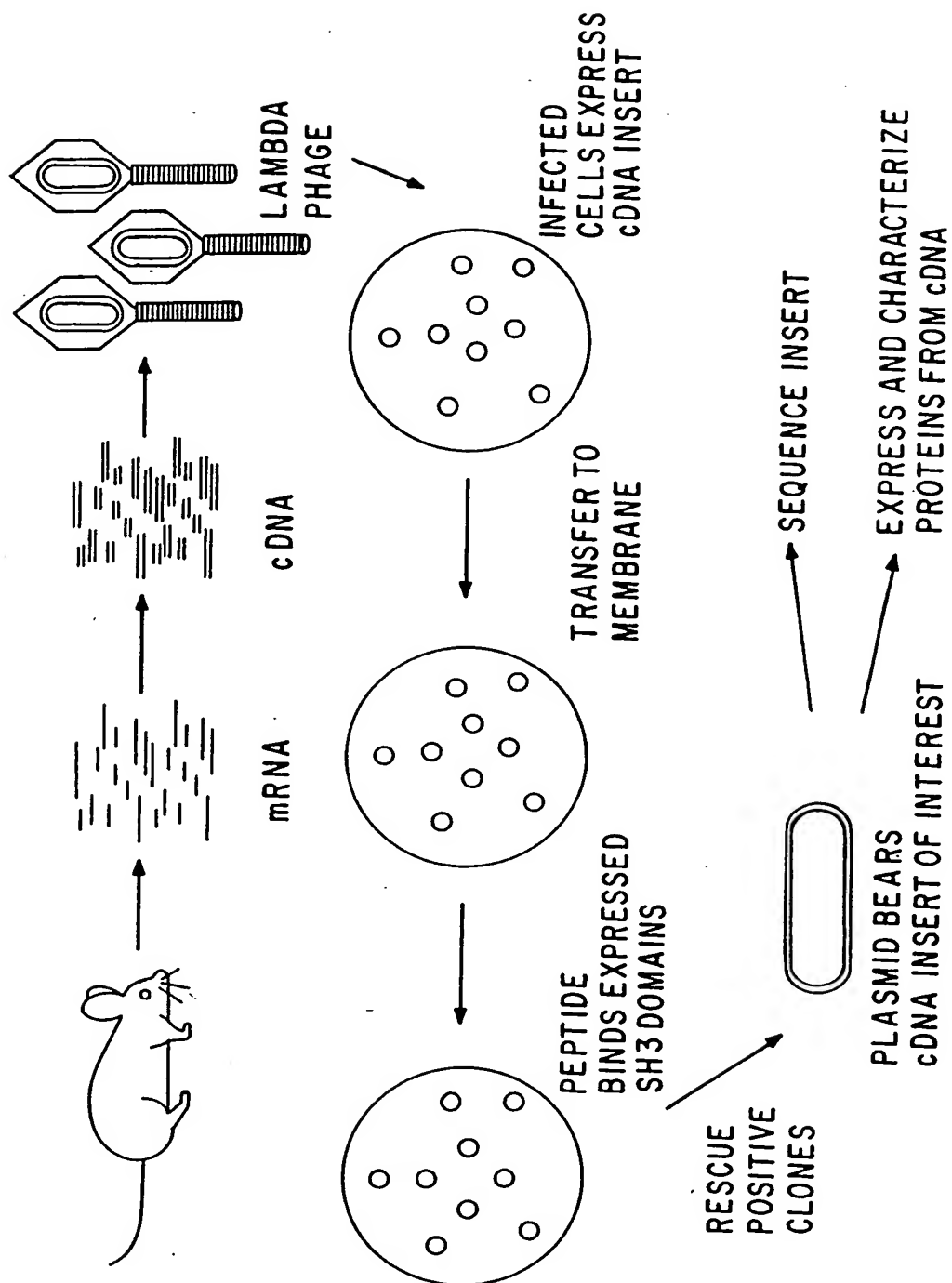


FIG. 3

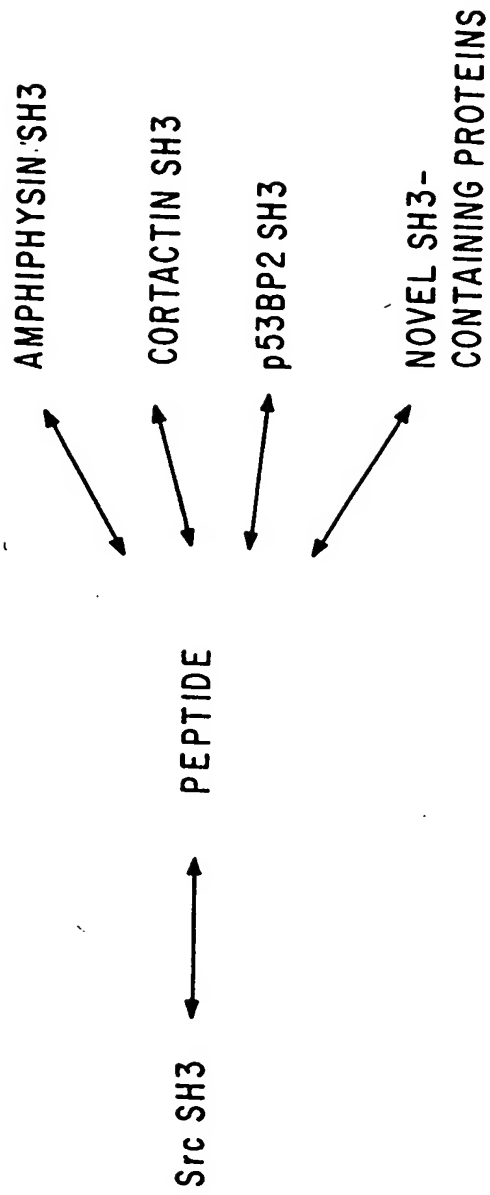
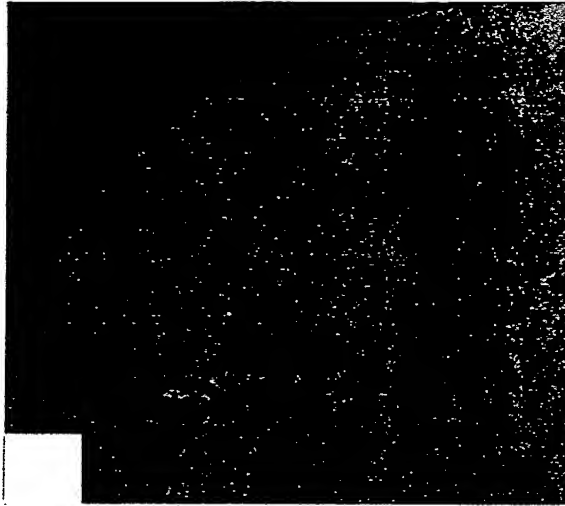
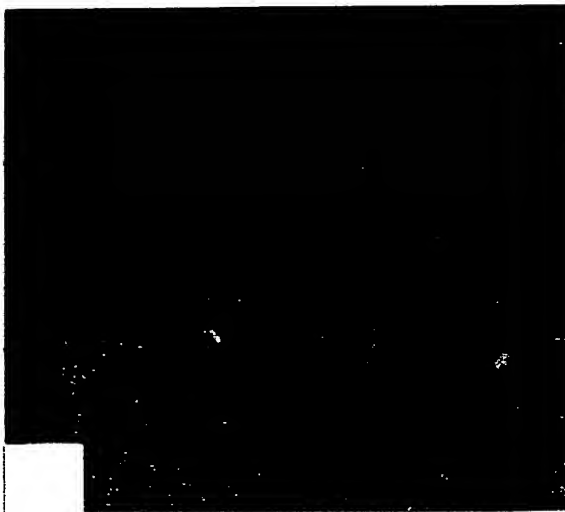


FIG. 4



**FIG. 5A**



**FIG. 5B**

		SEQ. ID NO.	
Sc_Fus1_Sh3:	TVI QDYE PRLTDE.....	IRISLG EKVKIL...A	.....THTD
Sc_Bob1_Sh3:	RAL FDYD KTKDGFSLQ	...ALSRFG DVLHVIDA	.....GDEE
Hs_Mpp1_Sh3:	RAQ FDYD PKKDNLIPCK	.EAGLK FATG DIIQIINK	.....DDSN
Hs_Zo1_Sh3:	RTH PHYE KESPY.....	...GLSFNKG EVFRAVDTL	.....NGKLS
Hs_Ncf1_Csh3:	VAI KAYT AV.EGD..E.	...VSLEG EAVEVIHK	.....LLDG
Hs_Rasgap_Sh3:	RAI LPYT KVPDTE..E.	...ISFLKG DMFIVHNE	.....LED
Sc_Sla_Nsh3:	RAV YAYE ..PQTP..EE	...LAIQED DLYLLQKSD	.....IDD
Sc_Bem1_Nsh3:	KAK YSYQ ..AQTS..KE	...LSFMEG EFFYV..SGD	.....EKD
Hs_Ncf2_Nsh3:	AHR VLFG FVPETK..EE	...LQMPG NIVFVL..KK	.....GND
Sc_Sla_Csh3:	RGI VQYD FMAESQ..DE	...LTIKSG DKYVILDDKK	.....SKD
Hs_Grb2_Csh3:	QAL FDPD ..POED..GE	...LGFRRG DFIHVMD..N	.....DPN
Hs_Nck_Csh3:	QAL YPFS ..SSND..EE	...LNFEKG DVMDVIEKPE	.....DPE
Mm_Tec_Sh3:	VAM YDFG ..ATEA..HD	...RLERG QEYILEKN	.....DLH
Hs_Atk_Sh3:	VAL YDYN ..PMNA..ND	...LQLRKG DEYFILEES	.....NLP
Hs_Ab1_Sh3:	VAL YDFV ..ASGD..NT	...LSITKG EKLRLVLGN	.....HNGE
Hs_Src_Sh3:	VAL YDYE ..SRTE..TD	...LSFKKG ERLQIVNNT	.....EGD
Hs_Fgr_Sh3:	IAL YDYE ..ARTE..DD	...LTFTKG EKPHILNNT	.....EGD
Hs_Fyn_Sh3:	VAL YDYE ..ARTE..DD	...LSFHGK EKQILNSS	.....EGD
Hs_Yes_Sh3:	VAL YDYE ..ARTT..ED	...LSFKKG ERFQIINNT	.....EGD
Mm_Fgr_Sh3:	VAL YDYE ..ARTG..DD	...LTFTKG EKPHILNNT	.....EYD
Hv_Stk_Sh3:	VAL YDYE ..ARIS..ED	...LSFKKG ERLQIINTA	.....DGD
Hs_Hck_Sh3:	VAL YDYE ..AIHH..ED	...LSFQKG DQWVVEES	.....GE
Hs_Lyn_Sh3:	VAL YPYD ..GIHP..DD	...LSFKKG EKMVLEE	.....GE
Mm_Blk_Sh3:	VAL PDYA ..AVND..RD	...LQVLKG EKQLVLRST	.....GD
Hs_Lck_Sh3:	IAL HSYE ..PSHD..GD	...LGFEKG EQLRILEQS	.....GE
Hs_Nck_Nsh3:	VAK FDYV ..AQOE..QE	...LOIKKN ERLWLLDDSK	.....SW
Sc_Sla_Msh3:	RAI YDYE QVQNAD..EE	...LTFHEN DVFDVFKKD	.....DAD
		CLVEKCNTRK	.....68
		QAR RVHSDSE	.....69
		OGR ..VEGSS	.....70
		AI RIGNHKE	.....71
		V IRKDDVTGY	.....72
		..MMVTNLR	.....73
		TVKKR VIGSD	.....74
		KASNP STGKE	.....75
		ATVMFNG.QK	.....76
		MCQLVDS.GK	.....77
		KG.A.CH.GQ	.....78
		KCRK.IN.GM	.....79
		RARD.KN.GQ	.....80
		RARD.KY.GW	.....81
		EAQT.KN.GQ	.....82
		LAHSLT.GQ	.....83
		EARSLSS.GK	.....84
		EARSLTT.GE	.....85
		EARSIAT.GK	.....86
		EARSLSS.GH	.....87
		YARSLIT.NS	.....88
		KARSLAT.RK	.....89
		KAKSLTT.KK	.....90
		LARSLVT.GR	.....91
		KAQSLTT.GQ	.....92
		VRNSM...NK	.....93
		LVKSTVS.NE	.....94

FIG. 6A

Hs_Hs1_Sh3:	VAL YDYQ	..GEGS..DE	....LSFDPD DVITDIEMV.	.....DEG	RG..RCH.GH	.....95
Sc_Abp1_Sh3:	TAE YDYD	..AAED..NE	....LTFVEN DKINIEFV.	.....DDD	LGELEKD.GS	.....96
Hs_Nck_Msh3:	YVK FNYN	..AERE..DE	....LSLKG TKIVMEKC.	.....SDG	RG..SYN.GQ	.....97
Hs_Vav_Sh3:	KAR YDFC	..ARDR..SE	....LSLKEG DIILNKK.	.....GQQ	WRGEIY..GR	.....98
Hs_Grb2_Nsh3:	IAK YDFK	..ATAD..DE	....LSFKRG DILKVLNEE.	.....CDQ	YKAELN..GK	.....99
Hs_Plcg2_Sh3:	KAL YDYK	..AKRS..DE	....LSFCRG ALIHNSKE	.....PG	WKGDTGT.RI	.....100
Hs_Plcg1_Sh3:	KAL FDYK	..AORE..DE	....LTFIKS AIIONVEKQ.	.....EG	WRGDYGG.KK	.....101
Ac_Mys1b_Sh3:	KAL YDYD	..AQTG..DE	....LTFKEG DTIIVHQKD.	.....PA	WEGELN..GK	.....102
Ac_Mys1c_Sh3:	RAL YDFA	..AENP..DE	....LTFNEG AVTVINKS.	.....NP	WEGELN..GQ	.....103
Dd_Mys1b_Sh3:	KAL YDYD	..ASST..DE	....LSFKEG DIIFIVQKD.	.....NG	TQGELKS.GQ	.....104
Hs_Ncf2_Csh3:	EAL FSYE	..ATQP..ED	....LEFQEG DIILVLSKV.	.....NE	LEGECK..GK	.....105
Hs_Ncf1_Nsh3:	RAI ADYE	..KTSG..SE	....MALSTG DVVEVVEKS.	.....ESG	FCQM..K.AK	.....106
Hs_Spectrin_Sh3:	MAL VDFQ	..ARSP..RE	....VTMKKG DVLTLLSSI.	.....NKD	KVEA..A.DH	.....107
Sc_Bem1_Csh3:	YAI VLYD	FKAKEA..DE	....LTTYVG ENLFICAH..	.....HNCE	IAKPIGRLGG	.....108
Sc_Cde25_Sh3:	VAA YDFN	YPIKKD..SS	..SQLSVQQG ETIIVLNKNS	SG	...DGL VIDD	.....109
Sp_Ste_Sh3:	.MR FQTT	AISDYENSSN	.PSFLKFSAG DTIIVIEVLE	D	CDG.....	.....110
Hs_Pf3ka_Sh3:	RAL VDYK	KEREEDIDLH	LGDILTVNKG SLVALGFSDG QEARPEEI		LNGYNETTGE	.....111

FIG. 6B

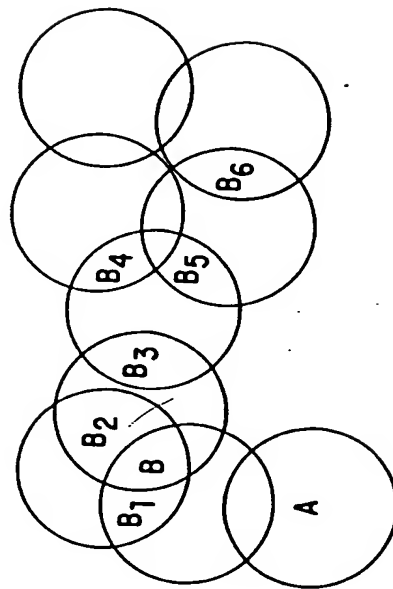
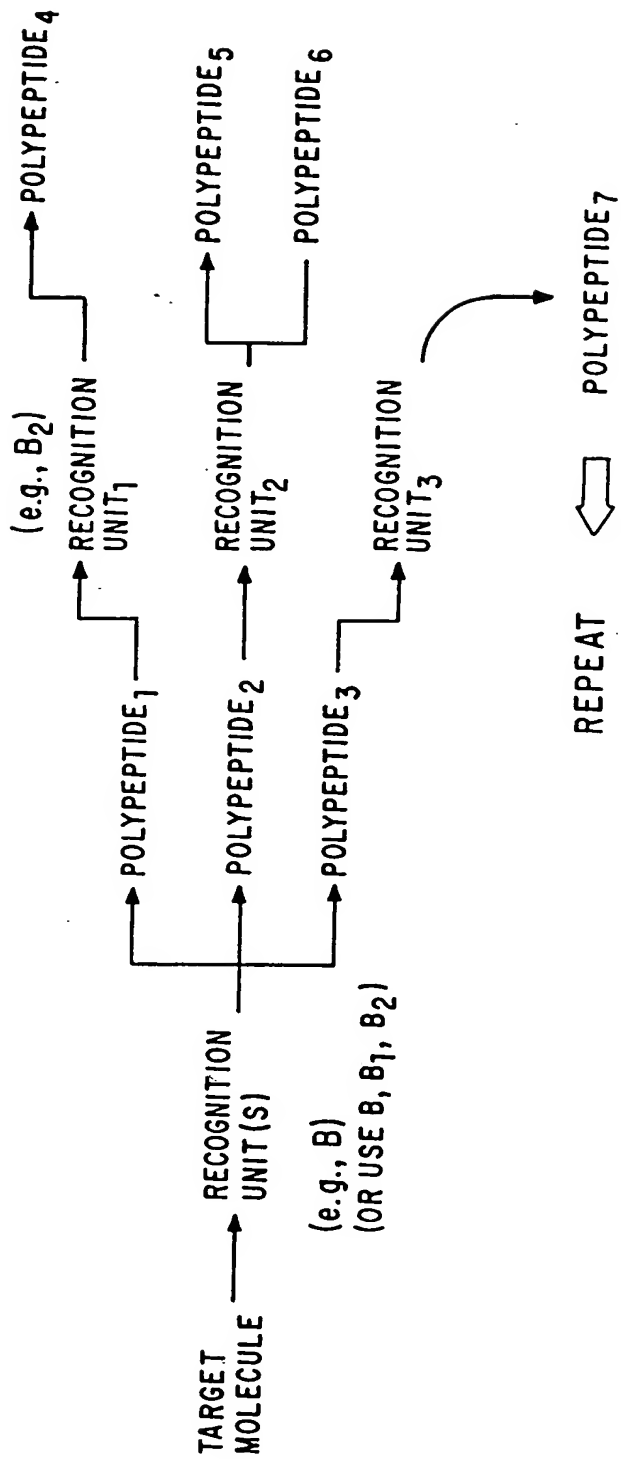


FIG. 7A

FIG. 7B



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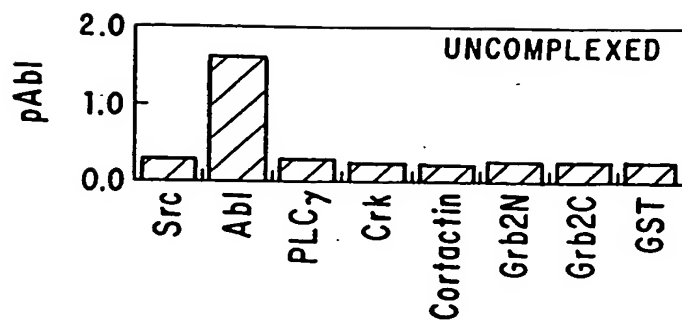


FIG. 8A

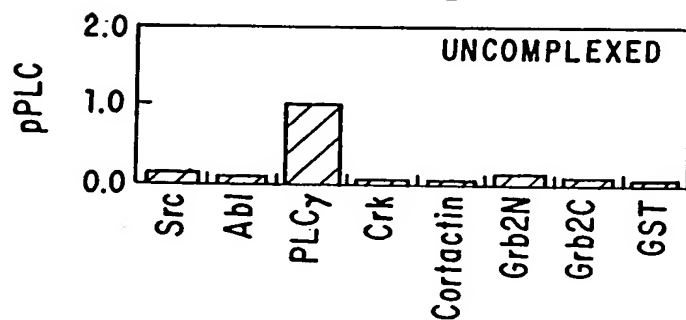


FIG. 8B

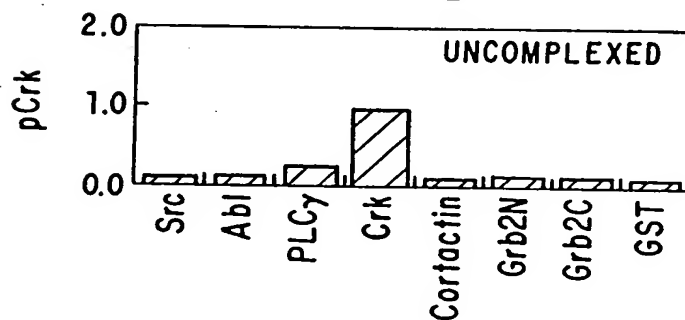


FIG. 8C

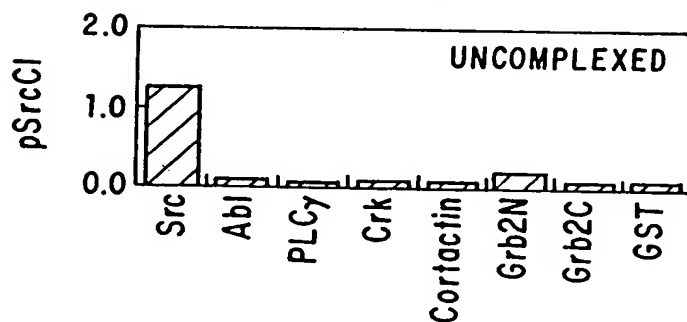


FIG. 8D

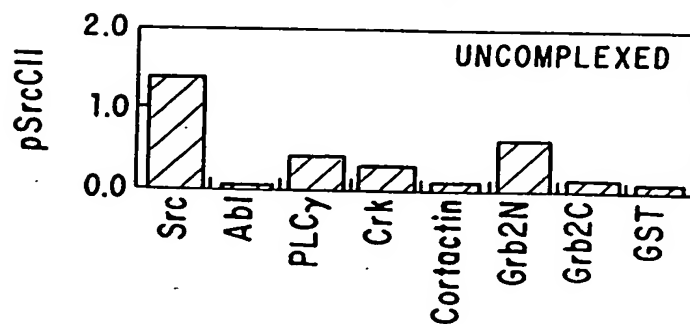


FIG. 8E

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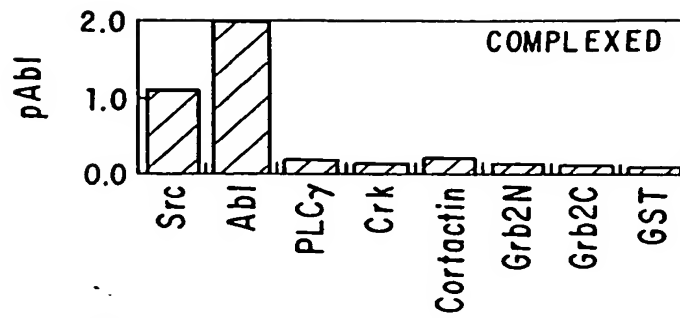


FIG. 8F

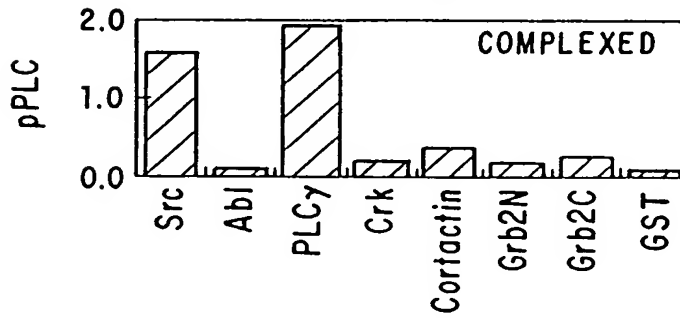


FIG. 8G

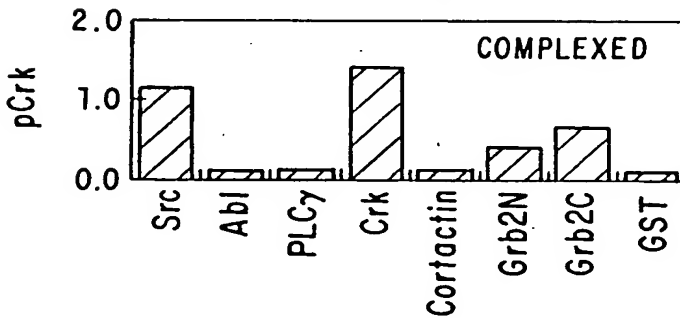


FIG. 8H

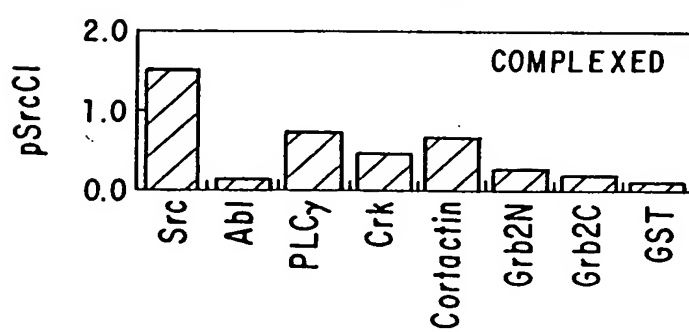


FIG. 8I

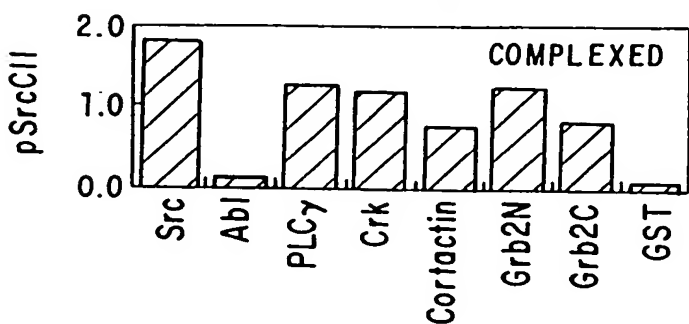


FIG. 8J

LIGAND: pSrcCII pCort pSrcCII pSrcCII  
 LIBRARY: Mouse Mouse Human1 Human 2

NAME	IDENTITY	#CLONES
—[AR]AR—[SH3]	SH3P1 p53bp2	1
—[P][SH3]ARARAR—	SH3P2 Novel	1
—[SH3]	SH3P3 Novel	1
—[HELIX]P—[SH3]	SH3P4 Novel	1
—[CRICR]CRICR[CRICR]—[HELIX]P—[SH3]	SH3P5 Cortactin	2
—[LIM][NR][NR]—[SH3]	SH3P6 MLN50	1
—[Drebrin][HELIX]—[P][E/P]—[SH3]	SH3P7 Novel	1
—[HELIX]P—[SH3]	SH3P8 Novel	1
—[Amphiphysin]—[SH3]	SH3P9 Novel	9
—[CRICR]CRICR—[P][E/P]—[SH3]	SH3P10 HSI	1
—[SH2]—[SH3]	SH3P11 Crk	2
—[SH3]—[SH3]	SH3P12 Novel	1
—[HELIX]P—[SH3]	SH3P13 Novel	2
—[SH3]	SH3P14 H74	8
—[SH3][SH2]—[TYR KINASE]	SH3P15 Lyn	1
—[SH3][SH2]—[TYR KINASE]	SH3P16 Fyn	2
—[SH3][SH3][SH3][SH3]	SH3P17 Novel	1
—[SH3][SH3][SH3]	SH3P18 Novel	2

FIG. 9

		SEQ. ID NO.
SH3P1	p53bp2	NKGTVVALWDYEAQNSDELSFHGDAITILRRKDN...ETEMMARLG.....DREGVVPKNLLGLY .....112
SH3P2	Novel	QVKVFRALYTFEPRTPDDELYFEEDGIIYITDMS.....DTSWKGTK.....GRTGLPSNYVAEQ .....113
SH3P3	Novel	HWTPYRAMYQYRPQNEDELELREGDRVDVWQC.....DDGFVGVSRRT.....QKFGTFPGNYVAPV .....114
SH3P4	Novel	DQPSCKALYDFEPENDGELGFREGDLITLTNQI.....DENWYEGMLH.....GQSGFFPLSYVQVL .....115
SH3P5	Cortactin	LGITAIALYDYQAAGDDEISFDPDDIITNIEMI.....DDGMRGVCK.....GRYGLFPANYVELR .....116
SH3P6	MLN50	GGKRYRAVYDYSAADEDEVSFQDGTIVNVQOI.....DDGMYGTVERT.....GDTGMLPANYVEAI .....117
SH3P7	Novel	QGLCARALYDYQAADDTISFDPENLITGIEVI.....DEGMRGYGPD.....GHFGMFPANYVELI .....118
SH3P8	Novel	DQPCCRALYDLEPENEGELAFKEGDIITLTNQI.....DENWYEGMLH.....GQSGFFPINYVEIL .....119
SH3P9	Novel, m	FMFKVQAQHDYTATDTDELQKAGDVVLVTFQNPPEEQDEGMLMGVKESDWNQHKLEKCRGVFPENFTERV .....120
	Novel, h	FMFKVQAQHDYTATDTDELQKAGDVVLVTFQNPPEEQDEGMLMGVKESDWNQHKLEKCRGVFPENFTERV .....121
SH3P10	HS1	AGISAIALYDYQGESELSFDPDDIITDIEMV.....DEGMRGQCR.....GHFGLFPANYVKLL .....122
SH3P11	Crk A	EAEYVRALDFNGNDEEDLPFKKGDIILTRDKP.....EEQWNAEDSE.....GKRGMIPVPYVEKY .....123
	B	RVIQKRVPNAYDKTALALEVGELVKVTKINV.....SGWMEGECN.....GKRGHFFFTHVRLL .....124
SH3P12	Novel A	EMRPARAKFDKFAQTLKELPLQKGDVVYIRQI.....DQNWYEGEHH.....GRVGIFPRTYIELL .....125
	B	EYGEATAKFNFGDTQVEMSFKRGERITLLRQV.....DENWYEGRIPGT.....SRQGITPITYVDVL .....126
	C	DLCSYQALYSYVPQNDDELELRQGDIVDMKEC.....DDGFVGVTSRRT.....RQFGTFPGNYVKPL .....127
SH3P13	Novel	DQPCCRGLYDFEPENEGELGFKEGDIITLTNQI.....DENWYEGMLR.....GESGFFPINYVEVI .....128
SH3P14	H74, m	TEVRVRALDYEGQEHDELSFKAGDELTKMEDE.....EQWCKGRLDN.....GQVGLYPANYVEAI .....129
	H74, h	KGVRVRALYDYGQEQDELSFKAGDELTKLGEED.....EQGMRGRIDS.....GQLGLYPANYVEAI .....130
SH3P15	Lyn	QGDIVVALYPYDGIHPDDLFSKKGKMKVLEE.....HGEWMAKSLLT.....KKEGFIPSNYVAKL .....131
SH3P16	Fyn	GVTLFVALDYEARTEDDLFSHKGEKFQILNSS.....EGDWMEARSLTT.....GETGIPSNYVAPV .....132
SH3P17	Novel A	KVVYVRALYPFESRSHDEITIQPGDIVMDESQTG.....EPGMLGGELK.....GKTGMFPANYAEKI .....133
	B	EGLQAQALYPWRACKDNHLNFKNDVITVLEQ.....QDMWVFGEVQ.....GQKGMFPKSYVKLI .....134
	C	GEEIAQVIASYTATGPEQLTAPGQLILTRKKN.....PGWMEGELQARGKK.....RQIGMFPANYVKLL .....135
	D	AVCQVIAMYDYTAQNDDDELAFNKGQIINVLNKE.....DPDWMKGEVN.....GQVGLFPSNYVKLT .....136

FIG. 10A

SEQ. ID NO.

SH3P18 Nove1 B VGEYIALPYSSVEPGDLTFTEGEEILVTQK.....DGEMMTGSIG.....DRSGIFPSNYVKPK .....137  
C KPEIAQVTSAYVAGSEQLSLAPGQLILILKKN.....TSGMWGELQARGKK.....RQKGMFPAASYVKLL .....138  
D PVCQVIGMYDYAANNEDELSFSKGQLINVMNKD.....DPDMNQGEIN.....GVTGLFPSNYVLEE .....139  
Src GVTTFVALYDYESRTETDLSFKKGERLQIVNNT.....EGDMWLAHSLTT.....GQTGYIPSNYVAPS .....140

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FIG. 10B

					SEQ. ID NO.
CLONE 5 P3-6		QVKVFRALYTFEPRTDPELYFEEDGIIYITDM	DTNWKGTS	GRTGLIPSNYVAEQ	.....204
CLONE 34 Crk LIKE		TGEEYIAGDFTAQQVGDLTFKKGEILLVIEKK	PDGWIIAKDAK	GNEGLVPRTYLEPY	.....205
CLONE 40 Ab1 BINDING		YLEKVAIYDYTKOKEDELSFQEGAIIVIKKN	DDGWYEGVMN	GVTGLSPGNVYESI	.....206
		PROTEIN			
CLONE 41 Nck LIKE A		LNIPAFVKFAYVAIEREDELVLKGSRTVMKEC	SDGWRGGSYN	GQIGWFPSNVYLEE	.....207
	Nck LIKE B	VLHVQTLYPFSSVTEEELNEFEKGETMEVIEKPENDPEWIKCKNAR		GOVGLVPKNYVVVL	.....208
CLONE 45 Nck A		EEVWVAKFDYVAQQEQELDIKKNERLWLLDD	SKSWRVNRSM	NKTGFVPSNVERK	.....209
	Nck B	LNMPAYVKFNMAEREDELSLIKGTKVIVMEKIC	SDGWRGGSYN	GQVGWFPSNVYTEE	.....210
	Nck C	VLHVQALYPFSSSNDDEELNFEKGDVMDVIEKPEN	DPEWIKCRKIN	GMVGLVPKNYVTVM	.....211
CLONE 53 NAB		DLFSYQALYSYIPQNDDELELRDGDIVDVMEKC	DDGWFVGTSRRT	KQFGTFPGNVKPL	.....212
CLONE 55 NOVEL		QGRKERARYDLEAAQDNELTFKAGEIMTVLDDS	DPNWKGETH	QGIGLFPSNFVTAD	.....213
CLONE 56 NOVEL		QGLCARALYDYQAADDTETISFDPENLITGIEVI	DEGWRGYGPD	GHFGMFPAHYVELI	.....214
CLONE 65 NOVEL	A	VLVNRALYPFEARNHDEMFSNGDIIQVDEKTVG	EPGWL YGSFQ	GNFGWFFPCNVYVKM	.....215
	B	VENLKAQALCSWTAKK DNHLNFSKHDIIITVLEQQ	ENFWWFGEVH	GGRGMFPKSYVKII	.....216
	C	VGEYIYALYPYSSVEPGDLTFTEGEEILVTQK	DGEWWTGSIG	DRSGIFPSNVYVKP	.....217
	D	KPEIAQVTSAYVASGS EQLSLAPGQLILILKKN	TSGWVQGELQARGKKRQKGMFPASWVKLL		.....218
	E	PVCQVIAMYDYAANNEDELVSFSGQLINVMNKD	DPDWVQGEIN	GVTGLFPSNVYKMT	.....219

FIG. 10C

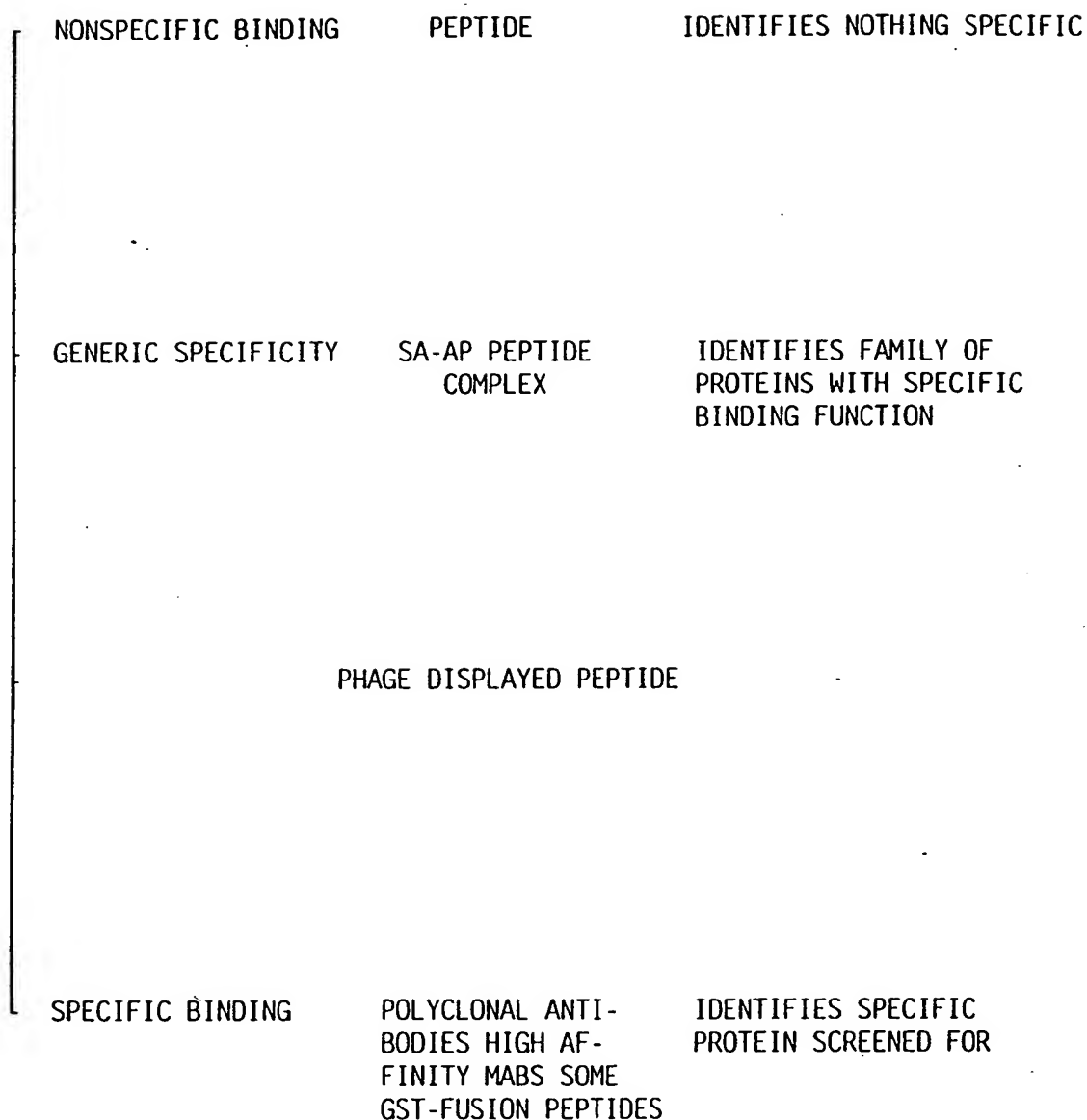


FIG. 11

SH3 DOMAIN CLONES																	
PEPTIDE	NAME	SEQUENCE	SEQ. ID NO.	5	11	12	13	14	18	34	40	41	45	46	53	55	65
SH3001	WBP-1	PGTPPPPYTVGPGY	141	-	-	-	-	-	-	-	-	-	-	-	-	-	-
TPPY	WBP-1	HGTPPPPYTVGP	142	-	-	-	-	-	-	-	-	-	-	-	-	-	-
QPPY	WBP-2	YVQPPPPPYPCPM	143	-	-	-	-	-	-	-	-	-	-	-	-	-	-
YPPE	WBP-2	PGYPYPPPEFY	144	-	-	-	-	-	-	-	-	-	-	-	-	-	-
WW005	WBP-1	PGTPAPPYTVGPGY	145	-	-	-	-	-	-	-	-	-	-	-	-	-	-
WW006	WBP-1	PGTPAPPYTVGPGY	146	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3002	K+ CHANNEL	DSGVRPLPPLPDGCV	147	-	-	-	+	+	-	++	-	-	-	-	-	-	-
bSH3003	K+ CHANNEL	VRPLPPLPEELPRRRPPPED	148	-	-	+	+	+	-	++	-	-	-	-	-	-	-
bSH3004	M4 AChr	PPPALPPPPRPVADK	149	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3005	$\beta$ 1 ADRENERGIC	APAPPPGPPAAAA	150	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3006	RasGop	GGGFPLPPPPYLPPLG	151	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3007	MEK	SISPRRPPGPRVSG	152	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3008	P Tyr PHOSP.	PPPEHI PPPPRKRILE	153	-	-	+	-	-	++	-	+	-	-	-	-	-	-
bSH3009	Fak	KEGERALPSIPKLAN	154	-	-	-	-	+	+	-	-	-	-	-	-	-	-
bSH3010	c-AbI	SRLKPAPPPPPAASAG	155	-	-	-	-	-	+++	-	-	-	-	-	-	-	-
bSH3011	c-Cbl	QASLPVPPRDLLLP	156	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3012	c-Cbl	PVPPTLRDLPPPPPPDRPYS	157	-	-	+++	++	++	-	+	-	-	-	-	-	-	-
bSH3013	Ca2+ CHANNEL	SDGGRNLPGTPVPAS	158	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3014	Ca2+ CHANNEL	RHSRRQLPPVPPKPRPLL	159	-	-	+	+	+	-	-	+	-	-	-	-	-	-
bSH3015	Nef	EKVGFPVTPQVPLRPMTY	160	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3016	MUS CADHERIN	PQPHRVLP TSPSDIA	161	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3017	AP2	ADFQPPYFP PPYQPTYPQS	162	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bSH3018	ACTIN BINDING	SSAAPPPPPRRATPEK	163	-	+	+++	-	-	+++	-	+++	-	-	+	+++	-	-

FIG.12A



SEQ.ID.NO

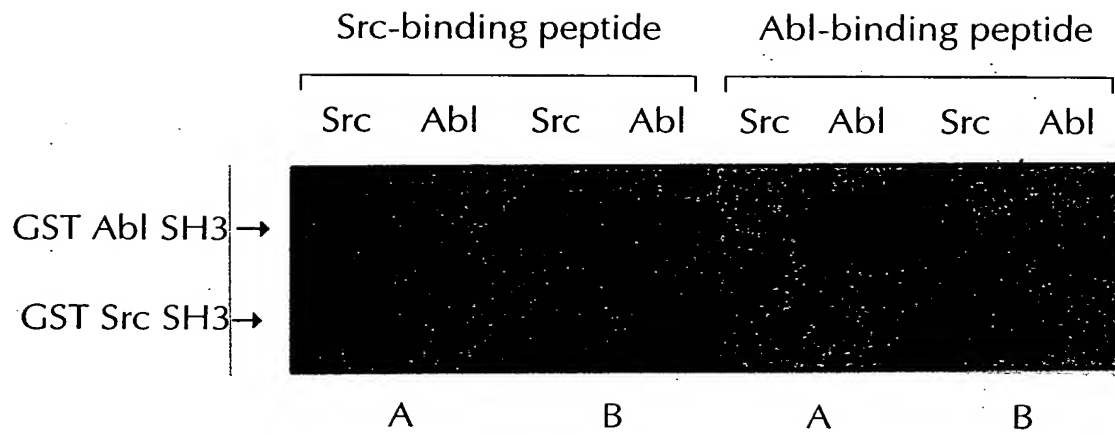
[illegible]

FIG. 12B

SEQ. ID NO.

[illegible]

FIG. 13

**FIG. 14**

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$\alpha$ GST Ab

Cortactin

Abl

Src

Src

Yes

Abl

Cortactin

p53bp2

PLC $\gamma$

Crk

Grb2 N

Grb2 C

Nck N

Nck M

Nck C

**FIG. 15**

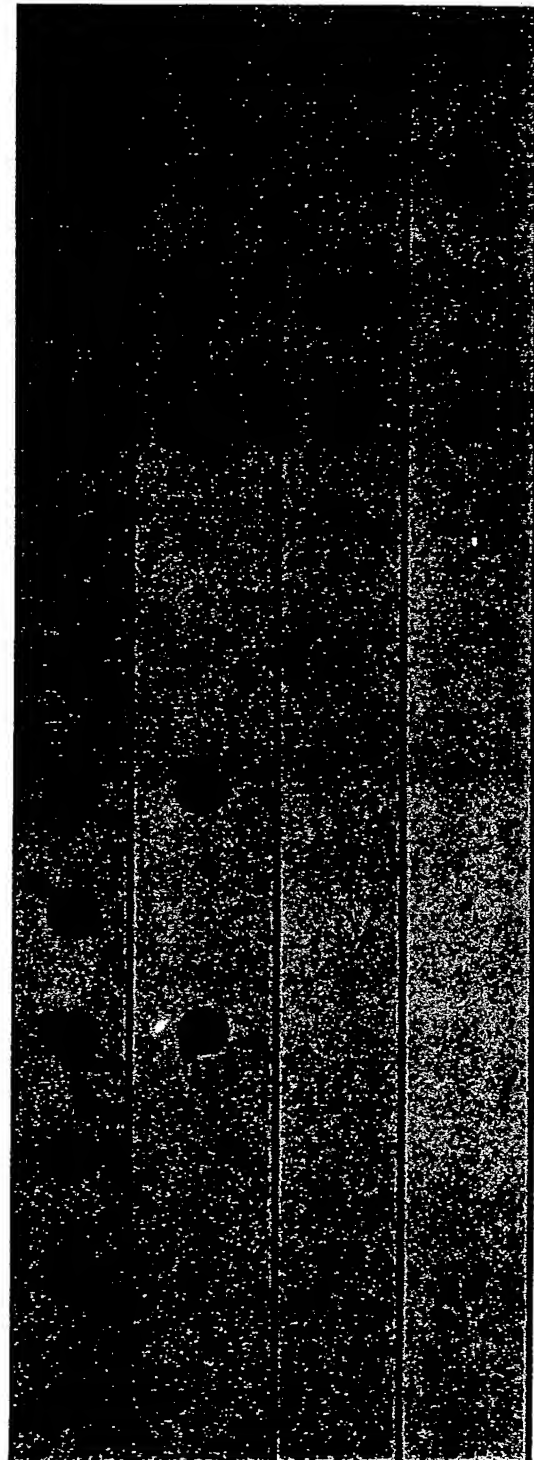
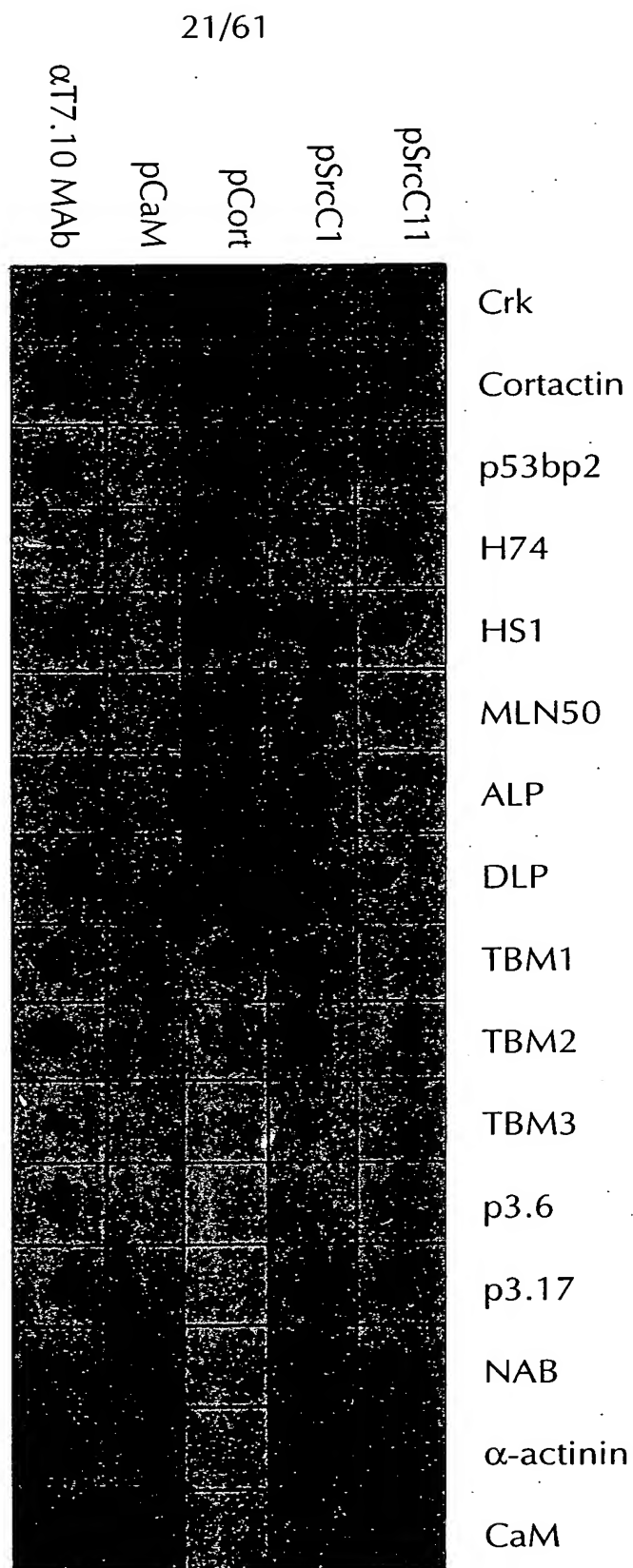


FIG. 16



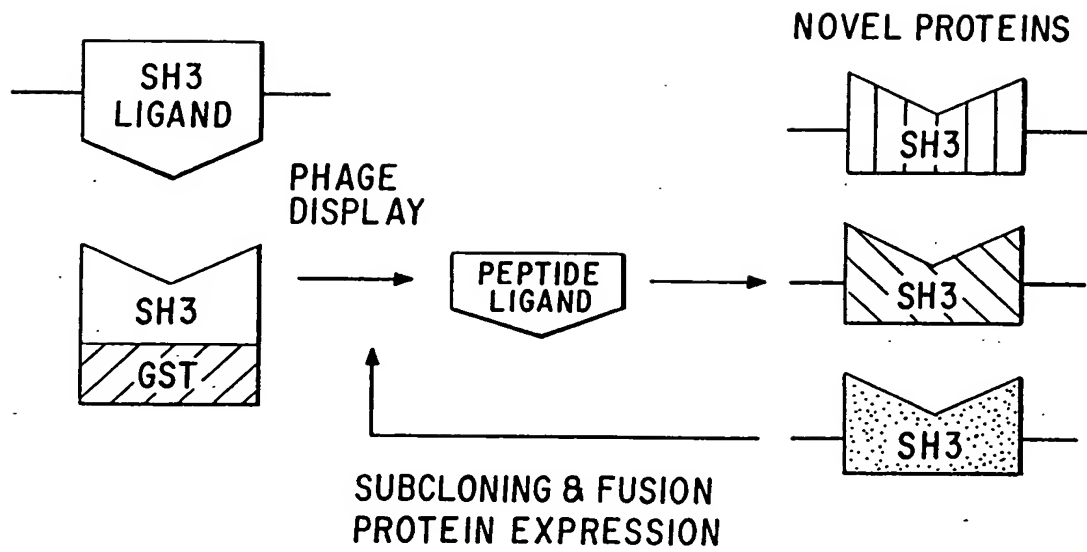


FIG. 17

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1   GTGAATGCTG CAGACAGTGA CGGATGGACA CCACTGCATT
41  GTGCTGCCTC TTGCAACAGT GTCCACCTCT GCAAGCAGCT
81  GGTGGAAAGT GGAGCCGCTA TCTTTGCCTC CACCATCAGT
121 GACATTGAGA CTGCTGCAGA CAAGTGTGAA GAGATGGAAG
161 AGGGATACAT CCAGTGTTCC CAGTTTCTGT ATGGGGTACA
201 AGAGAAGCTG GGAGTGATGA ACAAAGGCAC CGTGTATGCT
241 TTGTGGGACT ACGAGGCCCA GAACAGCGAT GAGCTGTCCT
281 TCCATGAAGG GGATGCCATC ACCATCCTGA GGCACAAAGA
321 TGA AACGAG ACCGAGTGGT GGTGGGCTCG TCTTGGGGAC
361 CGGGAGGGCT ACGTGCCCAA AAATTGCTG GGGTTGTATC
401 CACGGATCAA ACCCCGGCAG CGAACACTTG CCTGAACCCC
441 CTGGAGTACC ACAGTCTCGT TTGCTCCCAG GAGCTACTGG
481 AGGAGATCCC ACTGCCCTGG GAAACTGAA GCTAGGATGG
521 TCTCCTGGTG CTCACCTTAG CAGACAGTGT CCACAATGTG
561 AATCCCACTT CCCAGGTGAG GCCCTCTCCA GGCTGCAGGA
601 GCTGG (SEQ. ID NO:5)

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FIG. 18

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1   VNAADSDGWT PLHCAASCNS VHLCKQLVES GAAIFASTIS
41  DIETAADKCE EMEEGYIQCS QFLYGVOEKL GVMNKGTVYA
81  LWDYEAQNSD ELSFHEGDAI TILRRKDENE TEWWWARLGD
121 REGYVPKNLL GLYPRIKPRQ RTLA (SEQ ID NO:6)

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FIG. 19

```

1   SGCARSGAAA ASAGLAPSCR VRVGLPRLSL VAPCSAMSKP
41  PPKPVKPGQV KVFRLYTFE PRTPDELYFE EGDIIYITDM
81  SDTSWWKGTC KGRTGLIPSN YVAEQAESID NPLHEAAKRG
121 NLSWLRECLD NRVGVNGLDK AGSTALYWAC HGGHKDIVEV
161 LFTQPNVELN QQNKLGDAL HAAAWKGYAD IVQLLLAKGA
201 RTDLRNNEKK LALDMATNAA CASLLKKKQQ GTDGARTLSN
241 AEDYLDEDS D (SEQ ID NO:8)

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FIG 21

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1      GAATTCAA GCTCGGGTTG CGCGCGGTCC GGAGCGGCCG
41     CGGCCAGCGC AGGCTTGGCG CCCAGTTGTC GTGTGCGTGT
81     GGGGCTCCCG CGGCTGAGCC TGGTCGCTCC GTGTAGCGCC
121    ATGTCCAAGC CACCTCCCAA ACCGGTCAAA CCAGGGCAAG
161    TTAAAGTCTT CAGAGCTCTA TATACATTTG AACCCAGAAC
201    TCCAGATGAA TTATACTTTG AAGAAGGAGA CATTATCTAC
241    ATCACTGACA TGAGTGATAC CAGCTGGTGG AAAGGGACAT
281    GCAAGGGCAG AACAGGACTG ATCCCAGACA ACTATGTGGC
321    TGAGCAGGCA GAATCCATTG ACAATCCATT GCATGAAGCT
361    GCAAAAAGAG GCAACCTGAG CTGGTTGAGG GAGTGCTTGG
401    ACAACCGGGT GGGTGTGAAC GGCCTGGACA AAGCTGGAAG
441    CACAGCCCTG TACTGGGCCT GCCACGGTGG CCATAAAGAC
481    ATAGTGAGAG TTCTGTTTAC TCAGCCGAAT GTGGAGCTGA
521    ACCAGCAGAA TAAGCTGGGA GACACAGCTC TGCACGCGGN
561    TGCCTGGAAG GGTATGTCAG ACATTGTCCA GTTGCTACTG
601    GCAAAAGGTG CGAGGACAGA CTTGAGAAAC AATGAGAAGA
641    AGCTGGCCTT GGACATGGCC ACCAACGCTG CCTGTGCATC
681    GCTCCTGAAG AAGAAGCAGC AGGGAACAGA TGGGGCTCGA
721    ACGTTAAGCA ACGCCGAGGA CTACCTCGAT GACGAAGACT
761    CAGACTGATT CCCCCGGGG CCGCTTTGAT TGTTGCCTAA
801    ACTTCTTTTG CTTTTGCCAT TCCGGAGCCT GGGTTGTTTG
841    CCAGAAGAGT ATTGATAACT GTTGCTTTTA AAGTCTGTAT
881    GAGCGCGACA CTGCTGCACT GTGATCTGTG AGGAGTCGTT
921    GTGAGGGTGG CTCATTCTCA CCCACGCCTT GNCAATAAGT
961    GAAGAGATAC TTTGTTGTAT AAAATACATA TATGCTCACC
1001   AGGGTAAAAT AAACGAAAAA AANTTATTTT TATTTATCAA
1041   GCTAAAAAAA AAAAGCTTGG GCCCTNTTCT ATAGTGTCAC
1081   CTAAATACTA GCTTGANCCG GNTGCTAACA AAGCCCGAAA
1121   GGAAGCTGAG TTGCTGCTGC CACCGNTGAG CAATAACTAG
1161   CATANCCCCT TGGGGCCTCT AAACGGGTCT TGAGGGGTTT
1201   TTNGNTGAAA GGAGGANCTA TTTCCGATA ACCTGGNGTA
1241   ATAGGGAAGA GGCCCGNACC GATCGCCCTT CCCAACAGA

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(SEQ ID NO: 7)

FIG. 20



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1   .ACTCACGNC GGTGGAGTGG TACCGGATCG AATTCAAGCC GCATCACTGG
51  CACTGGACGC CAGGGCATCT TCCCTGCCAG CTACGTGCAG ATAAACCGAG
101 AGCCCCGGCT CAGGCTTTGT GATGATGGTC CCCAGCTCCC TGCATCACCT
151 AACCCGACAA CCACTGCTCA CCTAAGCAGC CACTCCCACC CCTCCTCAAT
201 ACCTGTGGAC CCCACTGACT GGGGAGGTCG AACCTCCCCT CGACGCTCCG
251 CCTTTCCCTT CCCCATCACC CTCCAGGAGC CCAGATCCCA AACCCAGAGT
301 CTCAATACCC CTGGACCAAC CCTGTCCCAT CCTCGAGCCA CCAGCCGTCC
351 CATAAACCTG GGACCCCTCT CCCCAAACAC AGAGATACAC TGGACTCCGT
401 ACCGGGCCAT GTACCAGTAC AGGCCCCAGA ATGAGGACGA GCTGGAACCT
451 CGAGAGGGGG ACCGTGTGGA TGTGATGCAG CAATGTGACG ATGGCTGGTT
501 TGTGGGTGTC TCCCGGCGAA CTCAGAAATT TGGGACATTC CCTGGAATT
551 ATGTAGCCCC AGTGTGAGTG GTCTCCATGG CAGTTTGGAG CCAACGAGGA
601 TCGGGAGGGG AGCAGTAGCA CTATGGGAGG GAGAGAGGCC TTCCATAGCC
651 TCCTCCCCAG GACCTGTGCT CCCAGCTTCT GCAGAGACCC CAGCAACTTT
701 CCCTCCAAGC CTCCTTGAAG TCCGATTCCC ACCCGCAAG TCACAGGCAT
751 TCCTTTGACA GCCCCCTTCA CCGCCCCTCA AATACAGACA TCTGCTTTCA
801 TGTGGGNAAA AAAAAAAAT TAAAGGTGG CCCTAT (SEQ ID NO:9)

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FIG.22

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1   RITGTGRQGI FPASYVQINR EPRLRLCDDG PQLPASNPNT
41  TTAHLSSHSH PSSIPVDPTD WGGRTSPRRS AFPFPITLQE
81  PRSQTQSLNT PGPTLSHPRA TSRPINLGPS SPNTEIHWTP
121 YRAMYQYRPQ NEDELELREG DRVDVMQQCD DGWFGVVSRR
161 TQKFGTFPGN YVAPV (SEQ ID NO:10)

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FIG.23

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1   MSVAGLKKQF HKATQKVSEK VGGAEGTKLD DDFKEMERKV
41  DVTSRAVMEI MTKTIEYLQP NPASRAKLSM INTMSKIRGO
81  EKGPGYPQAE ALLAEAMLKF GRELGDDCNF GPALGEVGEA
121 MRELSEVKDS LDMEVKQNF I DPLQNLHDKD LREIQHHLKK
161 LEGRRLDIFY KKKRQKIPD EELRQALEKF DESKEIAESS
201 MFNLLEMDIE QVSQLSALVQ AQLEYHKQAV QILQQVTVRL
241 EERIRQASSQ PRREYQPKPR MSLEFATGDS TQPNGGLSHT
281 GTPKPPGVQM DQPCCRALYD LEPENEGELA FKEGDIITLT
321 NQIDENWYEG MLHGQSGFFP INYVEILVAL PH
      (SEQ ID NO:12)

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FIG.25

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1 TNNNNYYMM SKYSKKGKKK KGKWMSGRTC GATTCAAGCC GACCAGCGGC
51 GGCCCGGCGA CCCCAGCCGC CTCTCCGCAT CTGCATCTGC ATCTGCCGGC
101 CGCGCAGCCT CCCGCATCCC ATCATGTCGG TGGCAGGGCT GAAGAAGCAG
151 TTCCACAAAG CCACTCAGAA AGTGAGTGAG AAGGTGGGAG GAGCGGAAGG
201 CACCAAGCTC GATGATGACT TCAAAGAGAT GGAGAGGAAA GTGGATGTCA
251 CCAGCAGGGC TGTGATGGAG ATAATGACAA AAACGATTGA ATACCTCCAA
301 CCCAATCCAG CTTCCAGGGC TAAGCTCAGT ATGATCAACA CCATGTGCGA
351 AATCCGCGGC CAAGAGAAGG GGCCAGGCTA CCCTCAGGCG GAAGCACTGC
401 TGGCAGAGGC CATGCTCAAG TTCGGCAGGG AGCTGGGTGA TGATTGCAAC
451 TTTGGTCCTG CTCTCGGTGA GGTGGGAGAA GCCATGAGGG AGCTCTCGGA
501 GGTCAAGGAC TCATTGGACA TGGAAGTGAA GCAGAATTTT ATCGACCCCC
551 TTCAGAATCT TCATGACAAG GATCTGAGGG AGATTGAGCA TCATCTGAAA
601 AAGCTGGAAG GCCGACGCTT AGACTTTGGT TATAAGAAGA AGCGACAAGG
651 CAAGATTCCA GATGAAGAAC TCCGCCAAGC TCTGGAGAAA TTCGATGAGT
701 CTAAAGAAAT CGCCGAGTCG AGCATGTTCA ACCTCTTGGA GATGGATATA
751 GAACAGGTGA GCCAGCTCTC CGCACTTGTT CAGGCTCAGC TGGAGTACCA
801 CAAGCAGGCA GTGCAGATCC TGCAGCAGGT CACTGTCAGA CTGGAAGAAA
851 GAATAAGACA AGCTTCATCT CAGCCAAGAA GGGAAATATCA GCCCAAACCA
901 CGGATGAGCC TAGAGTTTGC CACTGGAGAC AGTACTCAGC CCAACGGGGG
951 TCTCTCCAC ACAGGCACAC CCAAACCTCC AGGTGTCCAA ATGGATCAGC
1001 CCTGCTGCCG AGCTCTGTAT GACTTGGAAC CTGAAAATGA AGGGGAATTG
1051 GCTTTTAAAG AGGGCGATAT CATCACACTC ACTAATCAGA TTGACGAGAA
1101 CTGGTATGAG GGGATGCTTC ATGGCCAGTC TGGCTTTTTC CCCATCAACT
1151 ATGTAGAAAT TCTGGTTGCT CTGCCCCATT AGGATCCTGT GCTGGCTGGC
1201 TCACCTCCTT CTGACCCAGA TAGTTAAGTT TAACCACTGC TTTGGTAATG
1251 CTGCTTCCAA TACATCACGA ATGCAGGCCG CAGTGGATGA GTCACCAAGC
1301 CCACACGTGC CCTGGGTTGA CCCGTGTGCT CCTCCAGGAG ACGCGGTGAT
1351 AGATGGTATC TTCCAAGGCC AGTGGGCCTG GTACATGCTT TAAACACCA
1401 TCTGAGACTA GCCAGGAGTC CCAGAAGTGG CTTACAGTT CTCAGGAGGC
1451 TGTGGTTCCT GGTAACATGC CTGTGAACCA CATGGCAGAA AAATCTCTCT
1501 CACTGAAGAT ATTGTCTCTC ACCCAGGGGC CATCTCAAGG TCTCCAGTTC
1551 TCCATTTACA GAGGAGAAAG TCCTTTTGTG TGCATTTTCC CTTCTAAAT
1601 ATGTGAGTCA CAGAATTGTT GGCAAAAACA TCCCCTCACC AGCAAGATGT
1651 CTGCTGGTTT AAGCAACTTG GTCTCTTGAT GCCATTAGCA AAAGTATTAA
1701 TTGTCCAAAG CACCTTTGTT CACTAATATC TATCTATCTA TCTATCTATC
1751 TATCTATCTA TCTATCTATC TATCTATCAT CTATCTACCT ACCTATCTAC
1801 CTATCATCTA TCTATCTATC ATCTATTATC TATCTATCTA TCTATCTATC
1851 NNTCNATCTA TCTATCTATC CATCTATCTA TCCATCATCT ATCTACCTAC
1901 CTATCTACTA TCCATCTATC TATCTATCCA TCATCTATCT ACCTACCTAT
1951 CTAATATCCA TCCATTTATC TATCTATCTA TCTATCTATC TATCTATCTA
2001 TCTCCCTCAT ACTTCTGAGA CATGGCCAGT TTTCTTCCCT CCCTGCTGTT
2051 AAGCACTTGG NAGATGAGGG GGGGGGTCCC ATTTNATTTT TGAGTGAGAT
2101 GGTGAGCAGG GTGTATGTTG GCTGTNNTNN GGGGGTGGCC CTA

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(SEQ ID NO:11)

FIG. 24

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1 CGGGCGCGGC GGGAGCCTGG TGGACCCTGC TTTGGCGGTA
41 ATCATTGATC ATCGCAGATG CCCTCATATC CACTTTGGAT
81 TCCTTGGATT CGGACAGACT CTGAACTGCT TTTCCAGCA
121 AAAGAGAAAG ATGTGGAAG CCTCTGCAGG CCATGCTGTG
161 TCCATCACGC AGGATGATGG AGGAGCTGAT GACTGGGAGA
201 CTGATCCTGA TTTTGTGAAT GATGTGAGTG AAAAGGAGCA
241 GAGATGGGGT GCTAAAACCG TGCAGGGATC GGGGCACCAG
281 GAACACATCA ACATTCACAA GCTTCGAGAG AATGTCTTCC
321 AAGAACACCA GACGCTCAAG GAGAAGGAGC TGGAAACGGG
361 ACCCAAGGCT TCCCACGGCT ATGGCGGGAA GTTCGGTGTG
401 GAGCAGGATA GGATGGACAG ATCAGCCGTG GGCCATGAGT
441 ACCAGTCGAA GCTTTCCAAG CACTGCTCAC AAGTGGACTC
481 GGTCCGGGGC TTCGGAGGCA AGTTCGGTGT CCAGATGGAC
521 AGGGTGGATC AGTCTGCTGT AGGCTTTGAA TACCAGGGGA
561 AACTGAGAA GCATGCCTCC CAGAAAGACT ACTCTAGTGG
601 CTTCGGTGGC AAATACGGTG TGCAAGCTGA CCGTGTAGAC
641 AAGAGTGCCG TGGGCTTTGA CTACCAGGGC AAGACGGAGA
681 AGCATGAGTC TCAGAAAGAT TACTCCAAAG GTTTTGGTGG
721 CAAATATGGG ATTGACAAGG ACAAGGTGGA TAAAGTGCT
761 GTGGGCTTTG AGTATCAAGG CAAGACAGAG AAGCACGAAT
801 CCCAGAAAGA CTATGTAAAA GGCTTTGGAG GAAAGTTTGG
841 TGTGCAGACA GACAGACAGG ACAAGTGTGC CCTTGGCTGG
881 GACCATCAGG AGAAGCTGCA GCTGCATGAA TCCCAAAAAG
921 ACTATAAGAC TGGTTTCGGA GGCAAATTTG GTGTTCAGTC
961 CGAGAGGCAG GACTCCTCCG CTGTGGGGTT TGATTACAAG
1001 GAGAGATTGG CCAAGCACGA GCCCCAGCAA GACTATGCCA
1041 AAGGATTCGG CGGGAAGTAT GGGGTGCAGA AGGATCGGAT
1081 GGACAAGAAT GCATCCACCT TTGAAGAAGT GGTCCAGGTG
1121 CCATCTGCCT ATCAGAAGAC TGTCCCCATT GAGGCCGTAA
1161 CCAGCAAAAC CAGTAATATC CGTGCTAACT TTGAAAACCT
1201 GGCAAAGGAG AGAGAGCAGG AGGACAGGCG GAAGGCAGAA
1241 GCCGAGAGAG CTCAGCGGAT GGCCAAAGAA AGACAGGAGC
1281 AGCAGGAGGC GCGCAGGAAG CTGGAAGAGC AAGCCAGAGC
1321 CAAGAAGCAG ACGCCCCCTG CATCCCCTAG TCCTCAACCA
1361 ATTGAAGACA GACCACCCTC CAGCCCCATC TATGAGGATG
1401 CAGCTCCGTT CAAGGCCGAG CCGAGCTACC GAGGTAGCGA
1441 ACCTGAGCCT GAGTACAGCA TCGAGGCCGC AGGCATTCTT
1481 GAGGCTGGCA GCCAGCAAGG CCTGACCTAT ACATCAGAGC
1521 CCGTGACGA GACTACAGAG GCTCCTGGCC ACTATCAAGC
1561 AGAGGATGAC ACCTACGATG GGTATGAGAG TGACCTGGGC
1601 ATCACAGCCA TCGCCCTGTA TGA CTACCAG GCTGCTGGCG

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FIG. 26A

1641 ATGATGAGAT CTCCTTTGAC CCTGATGACA TCATCACCAA  
1681 CATAGAAATG ATTGACGATG GCTGGTGGCG TGGGGTGTGC  
1721 AAGGGCAGAT ACGGGCTCTT CCCAGCCAAC TATGTGGAGC  
1761 TGCGGCAGTA GGGCTGCCAC CCAGAGCCTA CCGGCACCAG  
1801 CACAGGGTTC AACTACAGA GCATCTGCGT GTGTTTGAGT  
1841 TGGTTTCTGC TTCCGTTTCT GTTTTG

(SEQ ID NO:13)

FIG. 26B

29/61

1 MWKASAGHAV SITQDDGGAD DWETDPDFVN DVSEKEQRWG  
41 AKTVQGSQH EHINIHLRE NVFQEHQTLK EKELETGPKA  
81 SHGYGGKFGV EQDRMDRSV GHEYQSKLSK HCSQVDSVRG  
121 FGGKFGVQMD RVDQSAVGFE YQKTEKHAS QKDYSSGFGG  
161 KYGVQADRVD KSAVGFDYQG KTEKHESQKD YSKGFGGKYG  
201 IDKDKVDKSA VGFEYQKTE KHESQKDYVK GFGGKFGVQT  
241 DRQDKCALGW DHQEKQLLHE SQKDYKTGFG GKFGVQSERQ  
281 DSSAVGFDYK ERLAKHEPQQ DYAKGFGGKY GVQKDRMDKN  
321 ASTFEEVVQV PSAYQKTUPI EAVTSKTSNI RANFENLAKE  
361 REQEDRRKAE AERAQMAKE RQEQEEARRK LEEQARAKKO  
401 TPPASPSQP IEDRPPSSPI YEDAAPFKA PSYRGSEPEP  
441 EYSIEAAGIP EAGSQGLTY TSEPVYETTE APGHYQAEDD  
481 TYDGYESDLG ITAIALYDYQ AAGDDEISFD PDDIITNIEM  
521 IDDGWWRGVC KGRYGLFPAN YVELRQ (SEQ ID NO:14)

FIG. 27

1 AAGCAGTCCT TCACCATGGT GGCCGACACT CCGGAAAACC TCCGCCTCAA  
51 GCAACAGAGC GAGCTGCAGA GTCAGGTGCG CTACAAGGAG GAGTTTGAGA  
101 AGAATAAGGG CAAAGGTTTC AGCGTGGTGG CAGACACGCC TGAGCTGCAG  
151 AGAATCAAGA AGACCCAGGA CCAGATCAGC AATATCAAAT ACCATGAGGA  
201 GTTTGAGAAG AGCCGCATGG GGCCAGTGAG AGGAGAAGGG GTGGAACCCAG  
251 AGCGCCGAGA AGCCAGGAC AGCAGCAGCT ACCGGAGGCC CACAGAGCAG  
301 CAGCAGCCGC AGCCTACCA TATCCCGACC AGTGCCCCCG TGTACCAGCA  
351 GCCCCAGCAG CAGCAGATGA CCTCGTCCTA TGGTGGGTAC AAGGAGCCAG  
401 CAGCCCCTGT CTCCATACAG CGCAGTGCCC CAGGTGGCGG TGGGAAACGG  
451 TACCGTGCAG TGTATGACTA CAGCGCTGCC GACGAGGACG AGGTCTCCTT  
501 CCAGGATGGG GACACCATCG TCAATGTGCA GCAGATCGAT GACGGCTGGA  
551 TGTACGGGAC CGTAGAGCGC ACCGGTGACA CGGGGATGCT GCCAGCCAAC  
601 TACGTGGAGG CCATCTGAAC CCTGTGCCGC CCCGCCCTGT CTTCAATGCA  
651 TTCCATGGCA TCACATCTGT CCTGGGGCCT GACCCGTCCA CCCTTCAGTG  
701 TCTCTGTCTT TTAAGATCTT CAACTGCTTC TTTATCCCCG CCCCTCCAGC  
751 TTATTTTACC ATCCCAAGCC TTGTTCTGCC CCTGTCATGG GCTCCTTCCT  
801 CTGGCAGGTT TTCCCTTGGA CCAATCAACT GATTGATTTT TCTCTCTGGA  
851 TGGAACAGGC TGGGCACTCT GGGGAGGGCA GGATTGTTCT TAGCTAGGTA  
901 GACTCCCAGG GCTGGGCTGA ACTAGGAGAC CCACTAAGGA GATCAGTTTA  
951 GACTGGGTGC AGTGGAAC ACCCTTAATT CCCAGCGAAG GGAGTCAGAG  
1001 GCAGGCAGAT CTGTGACTTG GAAGCCAGCC TGGTCTACAT CGAGAGTTTC  
1051 AGGACAGCCA GAGCTATGTA GTGAGGCCCT GTCTCGGAGG AAGAGTGGGG  
1101 GTTGGTTAGC TCTCAGCTTC ACTTCCTGCC TTAGGCTCCT CAGAACCCCT  
1151 GGCCAGCTC CCCCAACTCC CTTCTCCTA GAGGTGGGGT GAGCTGTGC  
(SEQ ID NO:15)

FIG. 28

1 KQSFTMVADT PENLRLKQQS ELQSQVRYKE EFEKNKGKGF SVVADTPELQ  
 51 RIKKTQDQIS NIKYHEEF EK SRMGPSGGEG VEPERREAQD SSSYRRPTEQ  
 101 QQPQPHHIPT SAPVYQQPQQ QQMTSSYGGY KEPAAPVSIQ RSAPGGGGKR  
 151 YRAVYDYSAA DEDEVSFQDG DTIVNVQQID DGWMYGTVER TGD TGMLPAN  
 201 YVEAI (SEQ ID NO:16)

FIG. 29

1 ATGGCGGTGA ACCTGAGCCG GAACGGGCCG GCGCTGCAGG AGGCCTACGT  
 51 GCGCGTAGTC ACCGAGAAAT CCCCACC GA CTGGGCTCTT TTTACCTATG  
 101 AAGGCAACAG CAATGACATC CGTGTGGCTG GCACAGGAGA GGGAGGCCTG  
 151 GAGGAGCTGG TGAAGAGCT CAACAGCGGG AAGGTGATGT ACGCCTTCTG  
 201 CAGGGTGAAG GACCCCACT CCGGCCTGCC CAAGTTTGTC CTCATCAACT  
 251 GGACAGGAGA GGGTGTGAAT GATGTGCGGA AAGGAGCATG TGCCAACCAC  
 301 GTCAGCACCA TGGCCAATT CCTGAAGGGT GCCCAGTGA CCATCAATGC  
 351 CCGGGCCGAG GAGGATGTGG AGCCTGAGTG CATCATGGAG AAGGTTGCCA  
 401 AGGCCTCTGG GGCCAAC TAC AGCTTCCATA AGGAAAGCAC CTCCTTCCAG  
 451 GATGTAGGGC CGCAGGCCCC AGTGGGCTCT GTGTACCAGA AGACCAATGC  
 501 CATATCTGAG ATCAAGAGAG TCGGCAAGGA TAACTTCTGG GCCAAAGCTG  
 551 AGAAGGAAGA AGAGAACCGC CGCCTGGAGG AGAAGCGGCG TGCCGAAGAG  
 601 GAGCGGCAGC GGTGAGGA GGAGCGACGA GAGCGGGAGC TGCAGGAGGC  
 651 TGCCCGACGT GAGCAGCGCT ACCAGGAACA GCACAGATCA GCTGGAGCCC  
 701 CGAGCAGGAC AGGTGAGCCA GAGCAGGAAG CCGTTTCAAG GACCAGACAG  
 751 GAGTGGGAGT CTGCTGGGCA GCAGGCCCA CACCCACGAG AGATTTTCAA  
 801 GCAGAAGGAA AGGGCAATGT CCACCACCTC TGTCACCAGC TGCAGCCGG  
 851 GCAAGCTGAG GAGCCCCTTC CTGCAGAAGC AACTCACTCA ACCAGAAACC  
 901 TCCTACGGCC GAGAGCCAC AGCTCCTGTC TCCCGCCTG CAGCAGGTGT  
 951 CTGTGAGGAG CCAGCGCCTA GCACTCTGTC TTCTGCCAG ACAGAAGAAG  
 1001 AACCTACATA TGAAGTACCC CCAGAGCAGG ACACCCTCTA TGAGGAACCA  
 1051 CCACTGGTAC AGCAGCAAGG GGCTGGCTCC GAACACATTG ACAACTACAT  
 1101 GCAGAGCCAG GGCTTCAGTG GACAAGGGCT GTGCGCCCGG GCCTTGATG  
 1151 ACTACCAGGC AGCTGATGAC ACCGAGATCT CCTTTGACCC TGAGAACCTA  
 1201 ATCACAGGCA TCGAGGTGAT TGACGAAGGC TGGTGGCGAG GCTATGGGCC  
 1251 TGACGGCCAC TTTGGCATGT TTCCTGCCAA CTACGTGGAG CTCATAGAGT  
 1301 GA (SEQ ID NO:17)

FIG. 30

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1  MAVNLSRNGP ALQEAYVRVV TEKSPTDWAL FTYEGNSNDI RVAGTGEGGL
51  EELVEELNSG KVMYAFCRVK DPNSGLPKFV LINWTGEGVN DVRKGACANH
101 VSTMANFLKG AHVTINARAE EDVEPECIME KVAKASGANY SFHKESTSFO
151 DVGPOAPVGS VYQKTNAISE IKRVGKDNFW AKAKEEEENR RLEEKRRAAE
201 ERORLEEERR ERELQEAARR EORYQEQRHS AGAPSRTGEP EQEAVSRTRO
251 EWESAGQQAP HPREIFKQKE RAMSTTSVTS SQPGKLRSPF LQKQLTQPET
301 SYGREPTAPV SRPAAGVCEE PAPSTLSSAQ TEEPTYEVP PEQDTLYEEP
351 PLVQQQGAGS EHIDNYMQSQ GFSGQGLCAR ALYDYQAADD TEISFDPENL
401 ITGIEVIDEG WWRGYGPDGH FGMFPANYVE LIE (SEQ ID NO:18)

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FIG. 31

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1  MSVAGLKKQF YKASQLVSEK VGGAEGTKLD DDFKDMEKKV DVTSKAVAEV
51  LVRTIEYLQP NPASRAKLTN LNTVSKIRGQ VKNPGYPQSE GLLGECMVRH
101 GKELGGESNF GDALLDAGES MKRLAEVKDS LDIEVKQNF I DPLQNLCDKD
151 LKIEQHHLKK LEGRRLDFDY KKKRQGKIPD EELRQALEKF EESKEVAETS
201 MHNLLTDIE QVSQLSALVD AQLDYHRQAV QILEELADKL KRRVREASSR
251 PKREFKPRPR EPFELGELEQ PNGGFPCAPA PKITASSSFR SSDKPIRMPS
301 KSMPLDQPS CKALYDFEPE NDELGFGFREG DLITLTNQID ENWYEGMLHG
351 QSGFFPLSYV QVLVPLPQ (SEQ ID NO:20)

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FIG.33

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1  MAEMGSKGVT AGKIASNVQK KLTRAQEKVL QKLGKADETK DEQFEQCVQN
51  FNKQLTEGTR LQKDLRTYLA SVKAMHEASK KLSECLQEVY EPEWPGRDEA
101 NKIAENNOLL WMDYHQKLVD QALLTMDTYL GQFPDIKSRI AKRGRKLV DY
151 DSARHHYESL QTAKKKDEAK IAKAEELIK AOKVFEEMNV DLQEELPSLW
201 NSRVGFYVNT FQSIAGLEEN FHKEMSKLNQ NLNDVLVSLE KQHGSNTFTV
251 KAQPSDNAPE KGNKSPSPPP DGSPAATPEI RVNHEPEPAS GASPGATIPK
301 SPSQPAEASE VVGGAQEPGE TAASEATSSS LPAVVVETFS ATVNGAVEGS
351 AGTGRDLPP GFMFKVQAQH DYTATDDEL QLKAGDVVLV IPFONPEEQD
401 EGWLMGVKES DWNQHKLEK CRGVFPENFT ERVQ (SEQ ID NO:22)

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FIG. 35

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1  TTNNCACTCA CCGTCCGTGG TNNNNSTMMC SGWYNKRNTK YRRKMSSKRW
51  YKWKKCRRKS GCGGCGCCGA CCTGCGCGCG GAGGAAAGAA GTCGGTTCGG
101 CGGCGCCGGC GGAAACCGGA GTTCGAGCGG GAGGCCTGAC GCGGCAGGC
151 GGCATGTCGG TGGCGGGGCT GAAGAAGCAG TTCTACAAGG CGAGCCAGCT
201 GGTCAAGCAG AAGGTTGGTG GGGCCGAAGG GACCAAACTG GATGATGACT
251 TTAAAGATAT GGAAGAAGAG GTGGATGTCA CCAGCAAGGC CGTGGCAGAG
301 GTGCTGGTCA GAACCATAGA ATATCTGCAG CCTAACCCAG CCTCGAGAGC
351 CAAGCTGACT ATGCTGAACA CCGTATCCAA GATCCGGGGC CAAGTGAAGA
401 ACCCTGGCTA CCCACAGTCA GAGGGTCTGT TGGGAGAGTG CATGGTTCGC
451 CATGGCAAGG AACTAGGTGG AGAGTCCAAC TTCGGTGATG CCCTGCTAGA
501 TGCAGGTGAG TCCATGAAGC GCCTGGCTGA GGTGAAGGAC TACTGGACA
551 TCGAGGTCAA GCAGAACTTC ATTGACCCAC TACAGAACCT GTGTGACAAG
601 GATCTGAAGG AGATCCAGCA CCACCTGAAG AAATTGGAGG GCCGCCGCCT
651 TGACTTTGAC TACAAGAAGA AGCGCCAGGG CAAGATCCCC GATGAGGAGC
701 TGCGCCAGGC CCTAGAGAAG TTCGAGGAGT CCAAGGAGGT GCGGAGAGCC
751 AGTATGCACA ACCTCCTGGA GACTGATATA GAGCAGGTGA GCCAGCTCTC
801 GGCCCTGGTG GATGCCCAGC TGGACTACCA CCGCAGGCA GTGCAGATCC
851 TGGAGGAGCT GGCTGACAAG CTGAAGCGCA GGGTTCGGGA AGCCTCCTCA
901 CGCCCCAAGC GGGAGTTCAA GCCCCGGCCC CGGGAGCCCT TTGAGCTTGG
951 AGAGCTGGAG CAGCCCAATG GGGGATTCCC CTGTGCCCCA GCACCTAAGA
1001 TCACAGCCTC CTCATCATTT AGATCGTCAG ACAAGCCCAT CAGGATGCCC
1051 AGCAAGAGCA TGCCACCCCT GGACCAGCCA AGCTGCAAGG CGCTTTATGA
1101 TTTTGAGCCA GAGAATGATG GCGAGCTGGG CTTCCGTGAG GGGGACCTCA
1151 TCACGCTTAC CAACCAGATC GACGAGAACT GGTATGAGGG GATGCTGCAC
1201 GGCCAATCAG GCTTCTTCCC ACTCAGCTAC GTGCAGGTGC TGGTGCCTCT
1251 GCCTCAGTGA CTGGGCCTTT ACACCGCTGC CAGTCACAGT GCAGCAGCAG
1301 TCTAATGCCA AGGTGCTCTA GAAACACTAA TGTTCTCTCA GGGGGGACTC
1351 CTCCCCACTC CCTCAGCCCT GGGGCCCCC TATCCTAAGA CTCGGAAAGG
1401 CCCACCCTGA GGTTCTATTG CCTTCCTGGT GGTATCAGCT TCCAGCTGTT
1451 TCAACCCTTC CCAGCCCGTT GCTGGCGATG GSCNNYGCC CCCTCTCTAG
1501 GCTCTCTAGA GGCAGGCAGG TCCTTGGAAT CCCAGCCTG CAAGCAGAGG
1551 CTGGCCAGCT CCCAGCTCA GCACACAGAC ACACCTGGCA CCTGCTGCTC
1601 ATGAAGAAGT GCACAAGGCA CAAATGTGTA CACTTCCCAT GGGACCACAG
1651 ACCCAGCTCA GCTCTGTTGA AGACCAAGCA CAAAGGCCTT GAAGAGTGGA
1701 CATTCCCAGG TCCCTGGCAC CTTCCCTTGA GCCAGCTCCA TTGCTACTTA
1751 TTCATGTGAC TGAAGCTGAC CACAGGCAGC TGGCAGGTCC TTTTTTCAAC
1801 CAGCAGGCTA GGCTGGCCAT AGACCCAGCT CTGCCTCACC CTGCCATGTT
1851 CCAGTAATGG AGGCCTCCAG CCTGGGCTCT ATTACATTCT TCTCTACAGC
1901 TGCCCCATAA CCCGTGGCTT ATCCCTGGCA CGTGGGGCCA CACCCACGC
1951 CCCCTGGATA GGCAACACTG TCCTGCTCCA GCCTGTGCTG ANATGAAGT
2001 TACTCCTAAT TTTTTTTTAA AAAAAAAGTA TTAAATNTCT CTTTCTATAT
2051 AAAANAAAGN TGGCCCTANN NGGA (SEQ ID NO:19)

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FIG. 32



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1 CCTCACTCGC TCTCCCCGCG CACGCTCCGT CTCCGTCAGT CCCCTGAGCT
51 GTTCTAGTGC GCGGCGTGGA GCCAGGGCTC AGGCTGGTGG AGCGGCCGGG
101 GCTGGAGGCT GGGAGTGCGG CGCGCACGGC CTCCCCGCGC CATTATCCGC
151 GCTCGCTTCG GCGGAGGCCG GCGCCAGGAT GGCAGAGATG GGGAGCAAGG
201 GGGTGACGGC GGGGAAGATC GCCAGCAACG TACAGAAGAA GCTGACCCGA
251 GCGCAGGAGA AGGTCCTGCA GAAACTGGGG AAGGCGGACG AGACGAAGGA
301 CGAGCAGTTT GAGCAGTGTG TCCAGAACTT CAATAAGCAG CTGACAGAGG
351 GTACCCGGCT GCAGAAGGAT CTTGCGACCT ATCTGGCTTC TGTAAAGCG
401 ATGCACGAAG CCTCCAAGAA GCTGAGTGAG TGTCTTCAGG AGGTGTACGA
451 GCCCGAGTGG CCTGGCAGGG ATGAAGCAAA CAAGATTGCA GAGAACAATG
501 ACCTACTCTG GATGGACTAC CACCAGAAGC TGGTGGACCA GGCTCTGCTG
551 ACCATGGACA CCTACCTAGG CCAGTTCCTT GATATCAAGT CGCGCATTGC
601 CAAGCGGGGG CGGAAGCTGG TGGACTATGA CAGTGCCCGG CACCACTATG
651 AGTCTCTTCA AACCGCCAAA AAGAAGGATG AAGCCAAAAT TGCCAAGGCA
701 GAAGAGGAGC TCATCAAAGC CCAGAAGGTG TTCGAGGAGA TGAACGTGGA
751 TCTGCAGGAG GAGCTGCCAT CCCTGTGGAA CAGCCGTGTA GGTTTCTATG
801 TCAACACGTT CCAGAGCATC GCGGGTCTGG AGGAAAACTT CCATAAAGAG
851 ATGAGTAAGC TCAATCAGAA CCTCAATGAT GTCCTGGTCA GCCTAGAGAA
901 GCAGCACGGG AGCAACACCT TCACAGTCAA GGCCCAACCC AGTGACAATG
951 CCCCTGAGAA AGGGAACAAG AGCCCGTCAC CTCCTCCAGA TGGCTCCCCT
1001 GCTGCTACCC CTGAGATCAG AGTGAACCAT GAGCCAGAGC CGGCCAGTGG
1051 GGCCTCACCC GGGGCTACCA TCCCAAGTC CCCATCTCAG CCAGCAGAGG
1101 CCTCCGAGGT GGTGGGTGGA GCCCAGGAGC CAGGGGAGAC AGCAGCCAGT
1151 GAAGCAACCT CCAGCTCTCT TCCGGCTGTG GTGGTGGAGA CCTTCTCCGC
1201 AACTGTGAAT GGGGCGGTGG AGGGCAGCGC TGGGACTGGA CGCTTGGACC
1251 TGCCCCCGGG ATTCATGTTT AAGGTTCAAG CCCAGCATGA TTACACGGCC
1301 ACTGACACTG ATGAGCTGCA ACTCAAAGCT GGCGATGTGG TGTGGTGAT
1351 TCCTTTCCAG AACCCAGAGG AGCAGGATGA AGGCTGGCTC ATGGGTGTGA
1401 AGGAGAGCGA CTGGAATCAG CACAAGGAAC TGGAGAAATG CCGCGGCGTC
1451 TTCCCGGAGA ATTTTACAGA GCGGCTACAG TGACGGAGGA GCCTTCCGGA
1501 GTGTGAAGAA CCTTTCCCCC AAAGATGTGT G (SEQ ID NO:21)

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FIG. 34

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1 GAATTCGTCG ACCCACGCGT CCGGTTTGAG CAGTGCGTCC
41 AGAATTTCAA CAAGCAGCTG ACGGAGGGCA CCCGGCTGCA
81 GAAGGATCTC CGGACCTACC TGGCCTCCGT CAAAGCCATG
121 CACGAGGCTT CCAAGAAGCT GAATGAGTGT CTGCAGGAGG
161 TGTATGAGCC CGATTGGCCC GGCAGGGATG AGGCAAACAA
201 GATCGCAGAG AACAACGACC TGCTGTGGAT GGATTACCAC
241 CAGAAGCTGG TGGACCAGGC GCTGCTGACC ATGGACACGT
281 ACCTGGGCCA GTTCCCCGAC ATCAAGTCAC GCATTGCCAA
321 GCGGGGGCGC AAGCTGGTGG ACTACGACAG TGCCCGGCAC
361 CACTACGAGT CCCTTCAAAC TGCCAAAAAG AAGGATGAAG
401 CCAAAATTGC CAAGGCCGAG GAGGAGCTCA TCAAAGCCCA
441 GAAGGTGTTT GAGGAGATGA ATGTGGATCT GCAGGAGGAG
481 CTGCCGTCCC TGTGGAACAG CCGCGTAGGT TTCTACGTCA
521 ACACGTTCCA GAGCATCGCG GGCTGGAGG AAAACTTCCA
561 CAAGGAGATG AGCAAGCTCA ACCAGAACCT CAATGATGTG
601 CTGGTCGGCC TGGAGAAGCA ACACGGGAGC AACACCTCCA
641 CGGTCAAGGC CCAGCCCAGT GACAACGCGC CTGCAAAAGG
681 GAACAAGAGC CCTTCGCCTC CAGATGGCTC CCCTGCCGCC
721 ACCCCCGAGA TCAGAGTCAA CCACGAGCCA GAGCCGGCCG
761 GCGGGGCCAC GCCCGGGGCC ACCCTCCCCA AGTCCCCATC
801 TCAGCCAGCA GAGGCCTCGG AGGTGGCGGG TGGGACCCAA
841 CCTGCGGCTG GAGCCCAGGA GCCAGGGGAG ACGGCGGCAA
881 GTGAAGCAGC CTCCAGCTCT CTTCTGCTG TCGTGGTGGA
921 GACCTTCCCA GCAACTGTGA ATGGCACCGT GGAGGGCGGC
961 AGTGGGGCCG GCGCTTGGA CCTGCCCCCA GGTTTCATGT
1001 TCAAGGTACA GGCCCAGCAC GACTACACGG CCACTGACAC
1041 AGACGAGCTG CAGCTCAAGG CTGGTGATGT GGTGCTGGTG
1081 ATCCCTTCC AGAACCCTGA AGAGCAGGAT GAAGGCTGGC
1121 TCATGGGCGT GAAGGAGAGC GACTGGAACC AGCACAAGGA
1161 GCTGGAGAAG TGCCGTGGCG TCTTCCCCGA GAACTTCACT
1201 GAGAGGGTCC CATGACGGCG GGGCCCAGGC AGCCTCCGGG
1241 CGTGTGAAGA ACACCTCCTC CCGAAAAATG TGTGGTTCTT
1281 TTTTTTGTTT TGTTTTCGTT TTTCATCTTT TGAAGAGCAA
1321 AGGGAAATCA AGAGGAGACC CCCAGGCAGA GGGGCGTTCT
1361 CCCAAAGATT AGGTCGTTTT CCAAAGAGCC GCGTCCCGGC
1401 AAGTCCGGCG GAATTCACCA GTGTCCTGAA GCTGCTGTGT
1441 CCTCTAGTTG AGTTCTGGCG CCCCTGCCTG TGCCCGCATG
1481 TGTGCCTGGC CGCAGGGCGG GGCTGGGGGC TGCCGAGCCA
1521 CCATGCTTGC CTGAAGCTTC GGCCGCGCCA CCCGGGCAAG
1561 GGTCTCTTT TCCTGGCAGC TGCTGTGGGT GGGGCCCAGA
1601 CACCAGCCTA ACCTGGCTCT GCCCGCAGA CGGTCTGTGT
1641 GCTGTTTGAA AATAAATCTT AGTGTTCAAA ACAAATGAA
1681 AAAAAAAAAA TGATAAAAAA AAAAAAAAAA AAAAAAAAAA
1721 AAAAGGGCGG CCGC (SEQ ID NO: 23)

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FIG. 36

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1 EFVDPRVRFE QCVQNFNKQL TEGTRLQKDL RTYLASVKAM
41 HEASKKLNEC LQEVYEPDWP GRDEANKIAE NNDLLWMDYH
81 QKLVDQALLT MDTYLGQFPD IKSRIAKRGR KLVDYDSARH
121 HYESLOTAKK KDEAKIAKAE EELIKAQKVF EEMNVDLQEE
161 LPSLWNSRVG FYVNTFQSIA GLEENFHKEM SKLNQNLNDV
201 LVGLEKQHGS NTSTVKAQPS DNAPAKGNKS PSPPDGSPAA
241 TPEIRVNHEP EPAGGATPGA TLPKSPSQA EASEVAGGTQ
281 PAAGAEQEPGE TAASEAASSS LPAVVVETFP ATVNGTVEGG
321 SGAGRLDLPP GFMFKVQAQH DYTATDTDEL QLKAGDVVLV
361 IPFQNPEEQD EGWLMGVKES DWNQHKLEK CRGVFPENFT
401 ERVP (SEQ ID NO:24)

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## FIG. 37

```

1 MWKSVVGHV SVSVETQGDD WDTDPDFVND ISEKEQRWGA KTIEGSGRTE
51 HINIHQLRNK VSEEHILKK KEESGPKAS HGYGGQFGVE RDRMDKSAVG
101 HEYVADVEKH SSQTDAAARGF GGKYGVERDR ADKSAVGFDY KGEVEKHASQ
151 KDYSHGFGGR YGVEKDKRDK AALGYDYKGE TEKHESQRDY AKGFGGQYGI
201 QKDRVDKSAV GFNEMEAPTT AYKKTTPIEA ASSGARGLKA KFESLAEERK
251 KREEEKAQQ MARQQERKA VVKMSREVQQ PSMPVEEPAA PAQLPKKISS
301 EVWPPAESHL PPESQPVRSR REYVPVSLPT RQSPLGNHLE DNEEPPALPP
351 RTPEGLQVVE EPVYEAAPEL EPEPEPDYEP EPETEPDYED VGELDRQDED
401 AEGDYEDVLE PEDTPSLSYQ AGPSAGAGGA GISAIALYDY QGEGSDELSF
451 DPDDIITDIE MVDEGWWRGQ CRGHFGLFPA NYVKLL (SEQ ID NO:26)

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## FIG. 39

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1 MAGNFDSEER SSWYWGRLSR QEAVALLQGQ RHGVFLVRDS STSPGDYVLS
51 VSENSRVSHY IINSSGPRPP VPPSPAQPPP GVSPSRLRIG DQEFDSLPAI
101 LEFYKIHLYD TTTLIEPVAR SRQSGVILR QEAEYVRAL FDFNGNDEED
151 LPFKKGDILR IRDKPEEQWW NAEDSEGKRG MIPVPYVEKY RPASASVSAL
201 IGGNQEGSHP QPLGGPEPGP YAQPSVNTPL PNLONGPIYA RVIQKRPVNA
251 YDKTALALEV GELVKVTKIN VSGQWEGECN GKRGHFPFTH VRLLDQQNPD
301 EDFS (SEQ ID NO:28)

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## FIG. 41

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1 CAGCCGCTGG AGGGGGCGCC TGGTGTAGAT GTGAAAAGCC GTAACCAGGA
51 ACCAGTAAAG ATGTGGAAGT CTGTAGTGGG GCATGATGTA TCGGTTTCCG
101 TGGAGACCCA GGGTGATGAC TGGGATACAG ACCCTGACTT TGTGAATGAC
151 ATCTCCGAGA AGGAGCAACG GTGGGGAGCC AAGACCATTG AGGGCTCTGG
201 ACGCACAGAG CACATCAACA TCCACCAGCT GAGGAACAAA GTGTCAGAGG
251 AGCACGACAT CCTCAAGAAG AAGGAGCTGG AATCGGGGCC TAAGGCATCC
301 CATGGCTATG GCGGTCAGTT TGGAGTGGAG AGAGACCGGA TGGACAAGAG
351 TGCCGTGGGC CACGAGTATG TTGCTGATGT GGAGAAACAC TCATCTCAGA
401 CTGATGCSGC CAGAGGCTTT GGGGGCAAAT ATGGAGTTGA GAGGGACCGG
451 GCAGACAAGT CAGCGGTGGG CTTTGACTAC AAAGGAGAAG TGGAAAAGCA
501 TGCATCTCAG AAAGATTACT CTCATGGCTT TGGTGGCCGC TACGGGGTAG
551 AGAAGGATAA ACGGGACAAA GCAGCCCTGG GATACGACTA CAAAGGAGAG
601 ACGGAGAAGC ACGAGTCTCA GAGAGATTAT GCCAAGGGCT TTGGTGGCCA
651 ATATGGAATC CAGAAAGACC GAGTGGATAA GAGTGCTGTT GGCTTCAATG
701 AAATGGAGGC CCAACCACG GCGTATAAGA AGACAACACC CATAGAAGCT
751 GCTTCCAGTG GTGCCCGTGG GCTGAAGGCA AAATTTGAGT CCCTGGCTGA
801 GGAGAAGAGG AAGCGAGAGG AAGAAGAGAA GGCACAGCAG ATGGCCAGGC
851 AGCAACAGGA GCGAAAGGCT GTGGTAAAGA TGAGCCGAGA AGTCCAGCAG
901 CCATCCATGC CTGTGGAAGA GCCAGCGGCA CCAGCCCAGT TGCCCAAGAA
951 GATCTCCTCA GAGGTCTGGC CTCCAGCAGA GAGTCACCTA CCGCCAGAGT
1001 CTCAGCCAGT GAGAAGCAGA AGGGAATACC CTGTGCCCTC TCTGCCACG
1051 AGGCAGTCTC CATTGCAGAA TCACTTGGAG GACAACGAGG AGCCCCCAGC
1101 TCTGCCCCCT AGGACCCCAG AAGGCCTCCA GGTGGTGGAA GAGCCAGTGT
1151 ACGAAGCAGC ACCCGAGCTG GAGCCGGAGC CAGAGCCTGA CTATGAGCCA
1201 GAGCCAGAGA CAGAGCCTGA CTATGAGGAT GTTGGGGAGT TAGATCGGCA
1251 GGATGAGGAT GCAGAGGGAG ACTATGAGGA TGTGCTGGAG CCCGANGACA
1301 CCCCTTCTCT GTCCTACCAA GCTGGACCCT CAGCTGGGGC TGGTGGTGCG
1351 GGGATCTCTG CTATAGCCCT GTATGATTAC CAAGGAGAGG GAAGCGATGA
1401 GCTTTCCTTT GATCCAGATG ACATCATCAC TGACATTGAG ATGGTGGATG
1451 AAGGCTGGTG GCGGGGCCAA TGCCGTGGCC ACTTTGGA CTTCCTGCA
1501 AACTATGTCA AGCTCCTCTA ATGACCAGCC CATTGTCTTC CGACTTCCCG
1551 AATTCGAAGC TGCTCTGCCT CCCTCTTCCC ACTCCATGGT ACTGCTGCAA
1601 GGACCTGGCT GAACATCATG AGATGCCTGA AGTTCTGGCA GTCTGTCTCC
1651 CGCCTCTTTA AGAGCTTTAG GTAGAATCGC TCCAGGTGGG GGTGGGGGTG
1701 GGGGTGGGAT CCCTCTGTCC CTCTGTGACC ACTCTTCCCT GAGGTAGCTC
1751 ATGAAATCAT CTTGCAGACC TGCCTCCTTC AGCCGCACCC CAGCTCTGCC
1801 AACCTTGCTC TAGAGTGCTG GGATTCCCTT GCCCCGACCC TGGGTGCCAG
1851 CCTAGAGGGG AGGCTCTCAC AGGGCTGCCT GATTGCCCCT GTTGTGCTTT
1901 TGCTCATTTT TCTTCCCTTA GCAGACAAAT TGGAACTGCC CTTCTGTTTA
1950 GTCCTAAAC TGAAAATAAA ATGAGACTGT GGCTAAAAA AAAAAAAAAA
2003 AAA (SEQ ID NO: 25)

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FIG. 38

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1   GGATCCCCGG AGCCGGTCCG CTGGGCGGGG CGCAGGGCTG GAGGGGCGCG
51  CGTGCCGGCG GCGGCCAGC GTGAAAGCGC GGAGGCGGCC ATGGCGGGCA
101 ACTTCGACTC GGAGGAGCGG AGTAGCTGGT ACTGGGGCCG CCTGAGCCGG
151 CAGGAGGCGG TGGCGCTATT GCAGGGCCAG CGGCACGGGG TGTTCTGGT
201 GCGGGACTCG AGCACCAGCC CCGGGGACTA TGTGCTTAGC GTCTCCGAAA
251 ACTCGCGCGT CTCCCACTAC ATCATCAACA GCAGCGGCCC GCGCCCTCCA
301 GTGCCTCCGT CGCCCGCTCA GCCTCCGCCG GGAGTGAGTC CCTCCAGGCT
351 CCGAATAGGA GATCAAGAAT TTGATTCATT GCCTGCTTTA CTGGAATTCT
401 AAAAAATACA CTATTTGGAC ACTACAACAT TGATAGAACC AGTGGCCAGA
451 TCAAGGCAGG GTAGTGGAGT GATTCTCAGG CAGGAGGAGG CAGAGTATGT
501 GCGGGCCCTG TTTGACTTTA ATGGGAATGA TGAAGAAGAT CTTCCCTTTA
551 AGAAAGGAGA CATCTGAGA ATCCGGGATA AGCCTGAAGA CGAGTGGTGG
601 AATGCAGAGG ACAGCGAAGG AAAGAGGGGG ATGATTCCTG TCCCTTACGT
651 GGAGAAGTAT AGACCTGCCT CCGCCTCAGT ATCGGCTCTG ATTGGAGGTA
701 ACCAGGAGGG TTCCCACTCA CAGCCACTGG GTGGGCGCGA GCCTGGGCCC
751 TATGCCCAAC CCAGCGTCAA CACTCCGCTC CCTAACCTCC AGAATGGGCC
801 CATTTATGCC AGGGTTATCC AGAAGCGAGT CCCTAATGCC TACGACAAGA
851 CAGCCTTGGC TTTGGAGGTC GGTGAGCTGG TAAAGGTTAC GAAGATTAAT
901 GTGAGTGGTC AGTGGGAAGG GGAGTGTAAT GGCAAACGAG GTCACCTCCC
951 ATTCACACAT GTCCGTCTGC TGGATCAACA GAATCCCGAT GAGGACTTCA
1001 GCTGAGTATA GCTCGACAGT TTGCTGACAG ATGGAACAAT CTGTTTTCCC
1051 CCAATTGCCA TCTATACAAT TTTCTTACAG GTGTCAAAGC AGTCTAGTTT
1101 ATATAAGCAT TCTGTTACCT GGGATCTTTT TTAAGACTGA ACTACTCCAT
1151 TCTCACTTGT ATTTACCATA TTCAGGTAC GAAACCGGAG GGCTTATGTG
1201 GTTAACTTCT GAGTTGGCAG TTTTAGGTGG TAGTGGCCGT GCCTGTATGA
1251 GAAGACGTAA ATACATTGCC TCCTTTCTTT TGGGCAAAC AGATCA

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(SEQ ID NO: 27)

## FIG. 40

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1   MSSECDVGSS KAVVNGLASG NHGPKDMDP TKICTGKGTV TLRASSSYRG
51  TPSSSPVSPQ ESPKHESKSD EWKLSSADT NGNAQPSPLA AKGYRSVHPS
101 LSADKPQGS LLNEVSSSHI ETDSQDFPPT SRPSSAYPST TIVNPTIVLL
151 QHNREQQKRL SSLSDPASE RAGEQDPVPT PAELTSPGRA SERRAKDASR
201 RVVRS AQDLS DVSTDEVGIP LRNTERSKDW YKTMFKQIHK LNRDDSDVH
251 SPRYSFSDDT KSPLSVPRSK SEMNYIEGK VVKRSATLPL PARSSSLKSS
301 PERNDWEPLD KKVDTRKYRA EPKSIYEYQP GKSSVLNNEK MSRDISPEEI
351 DLKNEPWYKF FSELEFGRPS SAVSPTPDIT SEPPGYIYSS NFHAVKRESO
401 GTPGGLASLE NERQIYKSVL EGGDIPLQGL SGLKRPSSSA STKDSSEPRH
451 FIPADYLEST EEFIRRRHDD KEKLLADQRR LKREQUEADI AARRHTGVIP
501 THHQFITNER FGDLLNIDDT AKRKSGLMR PARAKDFKA QTLKELPLQK
551 GDVVYIYRQI DQNWYEGEHH GRVGIFPTY IELLPPAEKA QPRKLAPVQV
601 LEYGEAIAKF NFNGDTQVEM SFRKGERITL LRQVDENWYE GRIPGTSRQG
651 IFPITYVDVL KRPLVKTPVD YIDL PYSSSP SRSATVSPQA SHHLSAGPD
701 LTESSEKNYVQ PQAQRRVTP DRSQPSLDC SYQALYSYVP QNDELELRD
751 GDIVDMKEC DDGWFVGTSR RTRQFGTFPG NYVKPLYL (SEQ ID NO: 30)

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## FIG. 43

```

1 CCTCACCGNN CCTGGTGTAG GTACCGGATC GAATTCAAGC GAAAAACAGA
51 GCGGGGCTGA CTGTAGCGTG GAGCGCGAGC CGGGCTGGAC GCGCGCAAGC
101 CCTTGCCGGG GACCCGCGAG GCAAGCAGTC TCCCTGTGGA GCGTCGTCCT
151 CCATCCCTGT AAGCACCGTT ACAGAGAATG AAACAAGGGC AGAAGTTACA
201 GAGCCCGTGA GGCATCTTCA AATAGAAGAC TGGAGACTAG AAASAGAATA
251 TTGCCAGGAG TTGGCATCCA TTGGAAGACC TTGAGATCCT CTCAGCTCAC
301 AACTCCAGGA CCGATGCATC TTCCCACCAC CTTGAAGCAC TGAGCCCTCC
351 AGAGCTGCAT CTGGGAAGAC TCGCCTGCCT CCAGCATGAG TTCTGAATGT
401 GATGTTGGAA GCTCTAAAGC TGTGGTGAAT GGCTTGGCAT CTGGCAACCA
451 TGGACCAGAC AAAGACATGG ACCCTACCAA AATCTGCACT GGGAAAGGAA
501 CAGTGACTCT TCGGGCCTCG TCTTCCTACA GGGGAACCCC AAGCAGCAGC
551 CCTGTGAGCC CCCAGGAATC TCCGAAGCAT GAAAGCAAGT CAGATGAATG
601 GAAACTTTCT TCCAGTGCAG ATACCAATGG CAACGCCAG CCCTCCCCAC
651 TTGCTGCCAA GGGCTATAGA AGTGTGCATC CCAGCCTTTC TGCTGACAAG
701 CCCCAGGGCA GTCCTTTACT AAACGAAGTT TCTTCTTCCC ACATTGAAAC
751 CGATTCCCAA GACTTCCCTC CAACAAGCAG ACCTTCGTCT GCCTACCCCT
801 CCACCACCAT CGTCAACCTT ACCATTGTGC TCCTGCAGCA CAATCGAGAG
851 CAGCAAAAGC GACTCAGTAG TCTTTCAGAT CCTGCCTCAG AGAGAAGAGC
901 GGGTGAGCAG GACCCAGTAC CAACCCAGC AGAACTACT TCGCCCGGCA
951 GGGCTTCTGA GAGAAGGGCA AAGGATGCTA GCAGACGGGT GGTGAGGAGC
1001 GCACAGGACC TGAGCGATGT GTCTACAGAT GAAGTGGGCA TTCCACTCCG
1051 GAATACCGAG CGATCGAAAG ACTGGTACAA AACTATGTTT AAACAGATCC
1101 ACAAAGTAA CAGAGATGAT GATTCTGATG TCCATTCCCC TCGATACTCC
1151 TTCTCTGATG ACACAAAGTC TCCCCTTTCT GTGCCTCGCT CAAAAAGTGA
1201 GATGAACTAC ATCGAAGGGG AGAAAGTGGT TAAGAGGTCC GCCACACTCC
1251 CCCTCCCAGC CCGCTCTTCC TACTCAAGT CCAGCCCGGA AAGAAACGAC
1301 TGGGAGCCCC TAGATAAGAA AGTGGATACG AGAAAATACC GAGCAGAGCC
1351 CAAAAGCATT TACGAATATC AGCCGGGCAA GTCTTCGGTC CTGACCAATG
1401 AGAAGATGAG TCGGGATATA AGCCAGAAG AGATAGATTT AAAGAATGAA
1451 CCTTGGTATA AATTCTTTTC GGAATTGGAG TTTGGGAGAC CGAGCTCAGC
1501 AGTCAGCCCG ACTCCAGACA TTACGTCAGA GCCTCCTGGA TATATCTATT
1551 CTTCCAACTT CCATGCAGTG AAGAGAGAAT CGGACGGGAC CCCCAGGGGT
1601 CTCGCTAGCT TGGAGAATGA GAGGCAGATC TATAAGAGTG TCTTGAAGC
1651 TGGCGACATC CCTCTTCAGG GCCTCAGTGG GCTCAAGCGA CCTTCCAGCT
1701 CAGCTTCCAC TAAAGATTCA GAGTCACCAA GACATTTTAT ACCAGCTGAT
1751 TACTTGGAGT CCACAGAAGA ATTTATTCGG AGACGGCACG ATGATAAAGA
1801 GAAACTTTTA GCGGACCAGA GACGACTTAA GCGCGAGCAA GAAGAGGCCG
1851 ATATTGCAGC TCGCCGCCAC ACAGGTGTCA TCCCGACTCA TCATCAGTTT
1901 ATACTAATG AGCGCTTTGG GGACCTCCTC AATATAGATG ATACGGCCAA
1951 AAGGAAATCT GGGTTAGAGA TGAGACCTGC TCGAGCCAAA TTTGACTTTA
2001 AAGCCCAGAC CCTGAAGGAG CTGCCTCTGC AGAAGGGAGA CGTTGTTTAC
2051 ATCTACAGAC AGATTGACCA GAACTGGTAT GAAGGTGAAC ACCATGGCCG
2101 GGTGGGAATC TTCCACGCA CCTATATCGA GCTTCTTCTT CCAGCTGAGA
2151 AGGCTCAGCC CAGAAAGTTG GCACCCGTAC AAGTTTTGGA ATATGGAGAA

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FIG. 42A

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2201 GCCATTGCAA AGTTTAACTT TAATGGAGAT ACACAAGTAG AAATGTCTTT
2251 CCGAAAGGGG GAGAGGATCA CGCTGCTCCG ACAGGTGGAT GAGAACTGGT
2301 ATGAAGGGAG GATTCCTGGG ACATCTCGCC AAGGCATTTT CCCTATCACC
2351 TATGTAGATG TGCTTAAGAG GCCATTGGTG AAAACCCCTG TGGATTACAT
2401 CGACCTGCCT TATTCTTCTT CCCCAGTCG CAGTGCCACT GTGAGCCCAC
2451 AGGCTTCTCA TCATTCATTG AGCGCAGGAC CTGATCTCAC AGAATCTGAA
2501 AAGAACTATG TGCAACCTCA AGCCCAGCAG CGAAGAGTCA CCCAGACAG
2551 GAGTCAGCCC TCACTGGATT TGTGTAGCTA CCAAGCGTTA TATAGTTATG
2601 TGCCACAGAA CGATGATGAG TTGGAACTCC GAGATGGAGA TATTGTTGAT
2651 GTCATGGAAA AATGTGACGA TGGATGGTTT GTTGGCACTT CGAGAAGGAC
2701 GAGGCAGTTT GGTACTTTTC CAGGCAACTA TGTA AACCT TTATATCTAT
2751 AAGAAGACTA AAAAGCACAG AGATTATTTT TTATCGGAGG ATGAAGCATC
2801 ATTCATGAAC TGGTCTCTTT ATTTAAGTAC TGAGTCAGTA AGAAAATAA
2851 TGCAGTTGGT AAAGAAAGAA TTCAAAGAAG GAACAGAGAA GTGTGTTTGA
2901 AACCCATTGT GTATCAGGGA TTA ACTATCT GCTGAAGACA TCTGTATTTA
2951 CATGACTGCT TCTGGGAGCT GCTCTAGCCC CCGCTGCTTG GGAATCTGA
3001 TCTGGAGCAT GTCCATGAGC AACATTAGCC AAAAAAAAAA GCTTGGGCCC
3051 TATTCTATAG TGTCACCTAA ATACTAGCTT GATCCGGCTG CTAACAAAGC
3101 CCGAAAGGAA GCTGAGTTGC TGCTGCCACC GCTGAGCAAT AACTAGCATA
3151 ACCCCTTGGG GCCTCTAAAC GGGTCTTGAG GGGTTTTTTG GCTGAAAGGA
3201 GGA ACTATAT CCGGATAACC TGGCGTAATA GCGAAGAGGC CCGCACC GAT
3251 CGCCCTTCCC AACAGTTGGG CAGCCTGAAT GGCGAATGGA CGCGCCCTGT
3301 AGCGGCGCAT TAAGCGCGGC GGGTGTGGTG GTTACGCGCA GGGTG

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(SEQ ID NO: 29)

FIG. 42B

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1 TTNNCACTCA CCGTCCTGGT GATGGTACCG GATCGAATTC AAGCGTGGCC
51 GTGGCCGTGG GGCGCGCGGG GACCGCCCGG GGTGCCCCGCT CCGCTCAGCG
101 TCCGGGCGCG GTGGTCCGGC GGAGCCCCGA GACCACCCCC GGGCGGGGCG
151 CCGCCGCGAT GTCGGTGGCT GGGCTCAAGA AGCAGTTCCA CAAAGCCAGC
201 CAGCTGTTTA GTGAAAAAAT AAGTGGTGCC GAAGGAACGA AGCTAGATGA
251 AGAATTTCTG AACATGGAAA AGAAAAATAGA TATCACCAGT AAAGCTGTTG
301 CAGAAATCCT TTCAAAGGCC ACAGAGTATC TCCAACCCAA TCCAGCATAC
351 AGAGCTAAGC TAGGAATGCT GAACACTGTG TCGAAGCTCC GAGGGCAGGT
401 GAAGGCCACC GGCTACCCAC AGACGGAAGG CTTGCTGGGG GACTGCATGC
451 TGAAGTATGG CAAGGAGCTC GGAGAAGACT CTGCTTTTGG CAACTCGTTG
501 GTAGATGTTG GTGAGGCCCT GAAACTCATG GCTGAGGTGA AAGACTCTCT
551 GGATATTAAT GTGAAGCAAA CTTTTATTGA CCCACTGCAG CTACTGCAAG
601 ACAAAGATTT AAAGGAGATC GGGCACCACC TGAGAAAGCT GGAAGGCCGT
651 CGCCTGGATT ATGATTATAA AAAGCGGCGG GTAGGTAAGA TCCCCGAGGA
701 AGAAATCAGA CAAGCAGTAG AGAAGTTTGA AGAGTCAAAG GAGTTGGCCG
751 AAAGGAGCAT GTTTAATTTT TTAGAAAATG ATGTAGAGCA AGTGAGCCAG
801 CTGGCTGTGT TTGTAGAGGC GGCATTAGAC TATCACAGGC AGTCCACAGA
851 GATCCTCCAG GAGCTGCAGA GCAAGCTGGA GTTGCGAATA TCTCTTGCAT
901 CCAAAGTCCC CAAGCGAGAA TTCATGCCAA AGCCTGTGAA CATGAGTTCC
951 ACCGATGCCA ATGGGGTCGG ACCCAGCTCT TCATCAAAGA CACCAGGTAC
1001 TGACACTCCC GCGGACCAGC CCTGCTGTCG TGGTCTCTAT GACTTTGAGC
1051 CAGAAAATGA AGGAGAATTA GGATTTAAAG AAGGGGACAT CATTACATTA
1101 ACCAATCAGA TAGATGAAAA CTGGTATGAA GGGATGCTTC GTGGGGAATC
1151 CGGCTTCTTC CCCATTAATT ACGTGGAAGT CATTGTGCCT TTACCTCCGT
1201 AAATGTGTCT TTTGGACCTA ACTTCAGAAC TGAAATGAAT TGGCACCAGT
1251 GCTCTCTCAG TGTGGTGTTT TGTGACANCC TCGCTCTCTG GCCCACTTAA
1301 TCACTTTTGT ATGTGTGTTT TCTTTATAAT GTATTTTGTG TCAATTTAAT
1351 TTGTATAACT GATTTCTTTG TCCTAACTCA TAAAAATAGT TTTCTTCTTG
1401 TTCTAAAAAG TCATTGGTTA AATGTATTTG CTTCTGTGTG CTAAACGAG
1451 TAAATTGCGC CCATTGGAAT GGCCTGGGTG GTCCTTGACT GCAGTGGGAA
1501 CGCACCCCTT GCAGCCATGA AAGCTAAAGG TTTGTTTCCT GACATTATTG
1551 ATGGCCTCTG GTCTTTTCCT GTTTTAAGCT TACCTGTGAA CAGCCCAATA
1601 AACNTGACAC ACTGTANAAT AANAAGGGTG GCCCNA (SEQ ID NO:31)

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FIG. 44



1 MSVAGLKKQF HKASQLFSEK ISGAEGTKLD EEFLNMEKKI DITSKAVAEI  
51 LSKATEYLQP NPAYRAKLG M LNTVSKLRGQ VKATGYPQTE GLLGDCMLKY  
101 GKELGEDSAF GNSLVDVGEA LKLMAEVKDS LDINVKQTFI DPLQLLQDKD  
151 LKEIGHHLRK LEGRRLDYDY KKRRVGKIPE EEIRQAVEKF EESKELAERS  
201 MFNFLENDVE QVSQLAVFVE AALDYHROST EILQELQSKL ELRISLASKV  
251 PKREFMPKPV NMSSTDANGV GPSSSSKTPG TDTPADQPCC RGLYDFEPEN  
301 EGELGFKEGD IITLTNQIDE NWYEGMLRGE SGFFPINYVE VIVPLPP

(SEQ ID NO:32)

## FIG. 45

1 MSGSYDEASE EITDSFWEVG NYKRTVKRID DGHRLCNDLM SCVQERAKIE  
51 KAYAQQLTOW AKRWRQLIEK GPQYGS LERA WGAMMTEADK VSELHQEVKN  
101 SLLNEDLEKV KNWQKDAYHK QIMGGFKETK EAEDGFRKAQ KPWAKKMKEL  
151 EAAKKAYHLA CKEERLAMTR EMNSKTEQSV TPEQQKKLVD KVDKCRQDVQ  
201 KTQEKYEKVL EDVGKTTPOY MEGMEQVFEQ COQFEEKRLV FLKEVLDDIK  
251 RHLNLAENSS YMHVYRELEQ AIRGADAQED LRWFRSTSGP GMPMNWPQFE  
301 EWNPDLPHTT AKKEKQPKKA EGATLSNATG AVESTSQAGD RGSVSSYDRG  
351 QTYATEWSDD ESGNPFGGNE ANGGANPFED DAKGVRVRAL YDYGQEQQDE  
401 LSFKAGDELT KLGEEDQGW CRGRLDGSQL GLYPANYVEA I

(SEQ ID NO:34)

## FIG. 47

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1 CGGGCTTGAG GCTGGGCCGC CGCCGCCGCC CGCTTTGCCA CCCGCCCCGC
51 TGATGGTGTC CGGTGCTCCG GCGCCCAGGG ACACAGACCG GGAGCAGGAC
101 CACTTCTCTC ACCTCCGGAT CTCTCCTGCT TCCGCAGCCT GTGAGCAGCA
151 GGCCTGCTAA CTGCAGATCC ACAACCGCAC AGCTCGCTAC AGGTGCACCA
201 TGTCTGGCTC CTACGATGAG GCCTCAGAGG AGATCACAGA TAGCTTCTGG
251 GAGGTGGGGA ACTACAAGCG GACGGTGAAG CGCATCGACG ATGGGCACCG
301 CCTGTGCAAC GACCTCATGA GCTGCGTGCA GGAGCGCGCC AAGATCGAGA
351 AGGCATACGC GCAGCAGCTC ACCGACTGGG CCAAGCGCTG GCGCCAGCTC
401 ATCGAGAAAG GTCCTCAGTA TGGCAGCCTG GAGCGGGCGT GGGGCGCCAT
451 GATGACAGAA GCAGATAAGG TCAGCGAGCT GCACCAGGAG GTGAAGAACA
501 GCCTGTGTAA TGAGGACCTG GAGAAAGTCA AGAACTGGCA GAAGGATGCC
551 TATCACAAGC AGATCATGGG TGGCTTCAAG GAGACGAAAG AGGCCGAGGA
601 TGGCTTCCGA AAGGCCCAGA AGCCCTGGGC TAAAAAGATG AAGGAGCTAG
651 AGGCGGCCAA GAAGGCCTAT CACTTGCTT GTAAGGAGGA AAGGCTGGCC
701 ATGACCCGGG AGATGAACAG TAAGACAGAG CAGTCGGTCA CCCCTGAACA
751 GCAGAAGAAA CTTGTGGACA AAGTGGACAA ATGCAGACAG GATGTGCAAA
801 AGACTCAGGA GAAGTATGAG AAGGTCCTGG AAGATGTGGG CAAGACCACA
851 CCACAGTACA TGGAGGGCAT GGAGCAGGTG TTTGAGCAGT GCCAGCAGTT
901 TGAGGAGAAG CGGCTGGTCT TCCTGAAGGA AGTCCTGCTG GATATCAAAC
951 GGCATCTCAA CCTAGCGGAG AACAGCAGCT ACATGCATGT CTACCGAGAA
1001 CTGGAGCAGG CCATCCGGGG GGCCGATGCC CAGGAGGACC TCAGGTGGTT
1051 CCGCAGCACC AGTGGCCCCG GGATGCCCAT GAACTGGCCG CAGTTCGAGG
1101 AGTGGAACCC AGACCTCCCG CACACCACTG CCAAGAAGGA GAAACAGCCT
1151 AAGAAGGCAG AGGGGGCCAC CCTGAGCAAT GCCACTGGGG CTGTAGAATC
1201 CACATCCCAG GCTGGGGACC GTGGCAGTGT TAGCAGCTAT GACCGAGGCC
1251 AAACATATGC CACCGAGTGG TCAGACGATG AGAGCGGAAA CCCCTTCGGG
1301 GGCAATGAGG CCAATGGTGG CGCCAACCCC TTCGAGGATG ATGCCAAGGG
1351 AGTTCGTGTA CGGGCACTCT ATGACTACGA CGGTCAGGAG CAGGATGAGC
1401 TCAGCTTCAA GGCCGGAGAT GAGCTACCA AGCTCGGAGA GGAAGACGAA
1451 CAGGGTTGGT GCCGCGGGCG GCTGGACAGC GGACAGCTGG GCCTCTATCC
1501 TGCCAACTAC GTTGACGCTA TATAGCTACC TTGCCACCC GACTCCTCTC
1551 AGTCCTTGTC CACCGCCTTC CACCCTTCCC CTCCCCCTTG CCATAGAGTT
1601 CCAGACATAT TTTCCCATCA AGCTTTTATT TTTTAAAAG TCAAAACAGA
1651 ACAAAAAAAAA AAAAAAAAAA GAAGAAATAC GAAGAGACAG CGTTTGCAGC
1701 CTACCTGGAG GCCGGGGGGG AGGGGGCTTA GGGTGATGGC CTCCCCACA
1751 GCGTGGGCAA GGATCTTGGG ACTAACCCAA TGTCACATCT GGTCTATAGA
1801 GTCCACCAAA GAGTCTCCTG AGTCTTGAGG GAGATCTTCT GGATCCTTCT
1851 ACCCTGTCTC GCTCTCCTAT CCCACCACAG CTGCCAGCAG CTGCCCATGT
1901 CACCTGAGCC TGGCTTCTA AACTCTCCTG TCCCCTCTCC TGTCCCCCTT
1951 CAACGCCCCC TTCTCTTAAA GGGCCCCCAA TCTTTAGTCT TCCACTCTGC
2001 CCTGGGGGTG CTTTCTCTT CCCAGCCCTG TCCAGTGAGG CTGGGGGAGA
2051 AGGCTGCGGA GGGGAGGGGA GTGTCTCTTC ACTCCCCAG ACATGAAGGC
2101 AGGTGAGTGG GAGGGAGTCA TGGCCTCCCT GGCATACAGG AGAGGAAGAA
2151 GGAGAACAGA CCATCTGACC AGGCTGTGCA ACACTCCCAA TGCCAAGCCC

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FIG. 46A

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2201 ATTTGAGGGA TGA AACCT AGCTGGGCCT GTGGGCAGAG GGCTCCTCCT
2251 CAGAGCCAAT GAGCATTTGC AGAGACCCTA CCTGTCTCTT TAGTCCTTGG
2301 CAATGGGCAA AGCCTCTTCC TTGAAAAGTC CAGGGCAAAG CCAGCAACAG
2351 TAGCAACCTC CTCTCACTCT GGGGAGGAGG CATTGGCCAC CCATCCCCCT
2401 CCCTTCATGG TCATTCAGAA ACGCCACAGC CCCTCCCATC CCCAATCACT
2451 GTGTCAGCAT CAGCCTTTGT GAAGACGGTC TACAAGGCTC TCACCTGGCC
2501 AACCTAGGAG ATTCAGGGGC TCAGGAACCT AGGAGATTCA GGGGCTTGGG
2551 GAACCTCCAC CTTGGCACTG TAAGGGGAAG CCAGCAGCTC AGGCTGGTGT
2601 GAGGAAGGAA CTCTGGATGG TCACTGTAGC TTTCTTCCTT GACCTTTTAG
2651 TCCCCAACAT CCCCTCTGAA TGCTGGCAGC ACCCCACCC CCACACACAC
2701 ACTCCCATTT CTCTAAGCCC GAGAGTCTTG AGTCTTCATT AAAGGATTCT
2751 GGGTGTGGGA GGGGACACAG GGCCTTGTGG TTGGGAAGCA GGTGGCAGGC
2801 TCTCCCTTGG GAGGATGGGG TGGGAAACGA AACAGGTCAA CCAAGACCTC
2851 TTACAGTGGA AAGTGGTCAG AGGCTGTTTC TTTGGACCTT TGGGAACACA
2901 GATTTGAGAA AGTCTCATAT TCACAGCTGG TGTCCGCTAG GCCTCTGGCC
2951 TACGGACACC CTCTGCCTTG TGAATCAGGT GACCTTTTGG GCCTCCAGGG
3001 AAAGAACAGG ACCACCATCC ATGTTCTCCG CGTCCCTTTA GCTCTCTGCT
3051 GCTTCTCCTG ACACTCAGGT CATGGACCCA AGCTTTGGGG TCCTGACCAC
3101 CGCCCCCCCC CACCCCCTT CTCTTGACTA GGCTGCAGCA GGGCCTTCTG
3151 TTGGGTCAGT CCTCCTCAGG GCCAGGAGCA GGAACCTAGC ACTCAAGAGA
3201 CAGGGCTGTA AGCACCCACT TCCCTGTCAC TGTTTGCCCT TGGGGCTTCA
3251 GCTGCAGCCC AGGTTGGGCC CTGGAGCCCT CAGAACCGGA AGCAGGATTC
3301 AAACCTCCCC TTCTCCACAG CCCCCCTGC CTCCCCAGAT GGTAGACATC
3351 CCCCAGCTCT TACCTTCACC CTCATCTCAG AAAGGCAAGA AGCCGCCATG
3401 TCCGCACCTT GGGGCCTGGG CTCCCCCTC TCTGTGCCAG CGGTTCCAG
3451 CACCTGGGGA GGGGCTGTGG CCTGACCAGA CCCCAGGCC ACCCCACATA
3501 GTATACTAGC TGCCCACTCT GGGGCAGGAA CTGGAAAATC CATCCCTTTT
3551 GAACAACCAC CTTCAATGAC CCCCCCATC TGGGACCAGA CTTGGTCCTC
3601 AAGTTATTCA GCACCCCCAG TGCAGGAGGG TCCTCCCCC ACCCCCCGAA
3651 GTCCCTGGAG CCCGGAGCAG AGCCCCACCT GTGATTCTG GTGTTAGGGC
3701 ACCTCAAACC TTGGGCTGGA CCACACCCT TCCCGCCATT TCCAGACCCC
3751 TACCTGTACT CCCAGTGCT CCCCAGGGGC CTCTTGATGC TGCACGGGAC
3801 CCTGCAGGGC TCGGTCAGTG ATGTGTTTTG TCCCCAGTTA ACCGCCATCC
3851 AGCGACCTGG TTCCAGGAGG AGCTCAGGTC ACCCCACCA CCGCCGCCAC
3901 TCGTCTGCC GCCCTAGGCT TTCAGACATC ATTAGTTCCG ACACTTGTGA
3951 AACTCCGAGA CGTGCCGTGG TCTCAGCAAT GCACCTGTTT TATACATGAT
4001 TGTGTAATTT AAAGGTATAT AAATACAAAT ATATATATTA TATCTATATC
4051 TATCAGTTGT GACCGTATGG CTGTCGATAA AACCAGAATT C

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(SEQ ID NO:33)

FIG. 46B

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1   GAATTCGTCG ACCCACGGTC CGGGAAGCCT TTCACAAGCA GATGATGGGC
51  GGCTTCAAGG AGACCAAGGA AGCTGAGGAC GGCTTTCGGA AGGCACAGAA
101 GCCCTGGGCC AAGAAGCTGA AAGAGGTAGA AGCAGCAAAG AAAGCCCACC
151 ATGCAGCGTG CAAAGAGGAG AAGCTGGCTA TCTCACGAGA AGCCAACAGC
201 AAGGCAGACC CATCCCTCAA CCCTGAACAG CTCAAGAAAT TGCAAGACAA
251 AATAGAAAAG TGCAAGCAAG ATGTTCTTAA GACCAAAGAG AAGTATGAGA
301 AGTCCCTGAA GGAACCTGAC CAGGGCACAC CCCAGTACAT GGAGAACATG
351 GAGCAGGTGT TTGAGCAGTG CCAGCAGTTC GAGGAGAAAC GCCTTCGCTT
401 CTTCCGGGAG GTTCTGCTGG AGGTTTCAGAA GCACCTAGAC CTGTCCAATG
451 TGGCTGGTTA CAAAGCCATT TACCATGACC TGGAGCAGAG CATCAGAGCA
501 GCTGATGCAG TGGAGGACCT GAGGTGGTTC CGAGCCAATC ACGGGCCGGG
551 CATGGCCATG AACTGGCCGC AGTTTGAGGA GTGGTCCGCA GACCTGAATC
601 GAACCCTCAG CCGGAGAGAG AAGAAGAAGT CCACTGACGG CGTCACCCTG
651 ACGGGCATCA ACCAGACAGG CGACCACTCT CTGCCGAGTA AGCCCAGCAG
701 CACCCTTAAT GTCCCGAGCA ACCCCGCCCCA GTCTGCGCAG TCACAGTCCA
751 GCTACAACCC CTTGAGGAT GAGGACGACA CGGGCAGCAC CGTCAGTGAG
801 AAGGACGACA CTAAGGCCAA AAATGTGAGC AGCTACGAGA AGACCCAGAG
851 CTATCCCACC GACTGGTCAG ACGATGAGTC TAACAACCCC TTCTCCTCCA
901 CGGATGCCAA TGGGGACTCG AATCCATTCTG ACGACGACGC CACCTCGGGG
951 ACGGAAGTGC GAGTCCGGGC CCTGTATGAC TATGAGGGGC AGGAGCATGA
1001 TGAGCTGAGC TTCAAGGCTG GGGATGAGCT GACCAAGATG GAGGACGAGG
1051 ATGAGCAGGG CTGGTGCAAG GGACGCTTGG ACAACGGGCA AGTTGGCCTA
1101 TACCCGGCAA ATTATGTGGA GCGATCCAG TGA (SEQ ID NO:35)

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FIG. 48

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1   RIRRPTVREA FHKQMMGGFK ETKEAEDGFR KAQKPWAKKL KEVEAAKKAH
51  HAACKEEKLA ISREANSKAD PSLNPEQLKK LQDKIEKCKQ DVLKTKEYE
101 KSLKELDQGT PQYMENMEQV FEQCQFEEK RLRFFREVLL EVQKHLDSL N
151 VAGYKAIYHD LEQSIRAADA VEDLRWFRAN HPGMAMNWP QFEWSADLN
201 RTLSRREKKK STDGVTLTGI NQTGDQSLPS KPSSTLNVPS NPAQSAQSQS
251 SYNPFEDDD TGSTVSEKDD TKAKNVSSYE KTQSYPTDWS DDESNNPFSS
301 TDANGDSNPF DDDATSGTEV RVRALYDYEG QEHDLSFKA GDELTKMEDE
351 DEQGWCKGRL DNGQVGLYP A NYVEAIQ (SEQ ID NO:36)

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FIG. 49

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1          AAAGGGAGG AGAGTGTCAA AAAGAAGGAT
30 GGCAGGAAA AAGGCAACA GGAAGCACAA GACAAGCTGG
70 GTCGGCTTTT CCATCAACAC CAAGAACCAG CTAAGCCAGC
110 TGTCCAGGCA CCCTGGTCCA CTGCAGAAAA AGGGTCCACT
150 TACCATTCTT GCACAGGAAA ATGTAAAAGT GGTGTATTAC
190 CGGGCACTGT ACCCCTTTGA ATCCAGAAGC CATGATGAAA
230 TCACTATCCA GCCAGGAGAC ATAGTCATGG TGGATGAAAG
270 CCAAAGTGA GAACCCGGCT GGCTTGGAGG AGAATTAATA
310 GGAAAGACAG GGTGGTTCCC TGCAAACTAT GCAGAGAAAA
350 TCCCAGAAAA TGAGGTTCCT GCTCCAGTGA AACCAGTGAC
390 TGATTCAACA TCTGCCCCTG CCCCCAACT GGCCTTGCCT
430 GAGACCCCCG CCCCTTTGGC AGTAACCTCT TCAGAGCCCT
470 CCACGACCCC TAATAACTGG GCCGACTTCA GCTCCACGTG
510 GCCCACCAGC ACGAATGAGA AACCAGAAAC GGATAACTGG
550 GATGCATGGG CAGCCCAGCC CTCTCTCACC GTTCCAAGTG
590 CCGGCCAGTT AAGGCAGAGG TCCGCCTTTA CTCCAGCCAC
630 GGCCACTGGC TCCTCCCCGT CTCCTGTGCT AGGCCAGGGT
670 GAAAAGGTGG AGGGGCTACA AGCTCAAGCC CTATATCCTT
710 GGAGAGCCAA AAAAGACAAC CACTTAAATT TTAACAAAAA
750 TGATGTCATC ACCGTCCTGG AACAGCAAGA CATGTGGTGG
790 TTTGGAGAAG TTCAAGGTCA GAAGGGTTGG TTCCCCAAGT
830 CTTACGTGAA ACTCATTTCA GGGCCCATAA GGAAGTCTAC
870 AAGCATGGAT TCTGGTTCTT CAGAGAGTCC TGCTAGTCTA
910 AAGCGAGTAG CCTCTCCAGC AGCCAAGCCG GTCGTTTCGG
950 GAGAAGAAAT TGCCCAGGTT ATTGCCTCAT ACACCGCCAC
990 CGGCCCCGAG CAGCTCACTC TCGCCCCTGG TCAGCTGATT
1030 TTGATCCGAA AAAAGAACCC AGGTGGATGG TGGGAAGGAG
1070 AGCTGCAAGC ACGTGGGAAA AAGCGCCAGA TAGGCTGGTT
1110 CCCAGCTAAT TATGTAAAGC TTCTAAGCCC TGGGACGAGC
1150 AAAATCACTC CAACAGAGCC ACCTAAGTCA ACAGCATTAG
1190 CGGCAGTGTG CCAGGTGATT GGGATGTACG ACTACACCGC
1230 GCAGAATGAC GATGAGCTGG CCTTCAACAA GGGCCAGATC
1270 ATCAACGTCC TCAACAAGGA GGACCCTGAC TGGTGGAAG
1310 GAGAAGTCAA TGGACAAGTG GGGCTCTTCC CATCCAATTA
1370 TGTGAAGCTG ACCACAGACA TGGACCCAAG CCAGCAATGA
      (SEQ ID NO: 37)

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FIG. 50

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1   KGRRVSKRRM ARKKANRKHK TSWVGFSINT KNQLSQLSRH
41  PGPLOKKGPL TISAQENVKV VYYRALYPFE SRSHDEITIQ
81  PGDIVMVDES QTGEPGWLGG ELKGKTGWFP ANYAEKIPEN
121 EVPAPVKPVT DSTSAPAPKL ALRETPAPLA VTSSEPSTTP
161 NNWADFSSTW PTSTNEKPET DNWDAAWAAP SLTVPSAGQL
201 RQRSAFTPAT ATGSSPSPVL GQGEKVEGLQ AQALYPWRAK
241 KDNHLNFNKN DVITVLEQQD MWWFGEVQGO KGWFPKSYVK
281 LISGPIRKST SMDSGSSESP ASLKRVASPA AKPVVSGEEI
321 AQVIASYTAT GPEQLTLAPG QLILIRKKNP GGWWEGELQA
361 RGKKRQIGWF PANYVKLLSP GTSKITPTEP PKSTALAAVC
401 QVIGMYDYTA QNDELAFNK GQIINVLNKE DPDWWKGEVN
441 GQVGLFPSNY VKLTTDM DPS QQ (SEQ ID NO:38)

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FIG. 51

```

1   GAATTCGCGG CCGCGTCGAC CAAGATCATT CCTGGGAGTG
41  AAGTAAACG GGAAGAACCA GAAGCTTTGT ATGCAGCTGT
81  AAATAAGAAA CCTACCTCGG CAGCCTATTC AGTTGGAGAA
121 GAATATATTG CACTTTATCC ATATTCAAGT GTGGAACCTG
161 GAGATTTGAC TTTCACAGAA GGTGAAGAAA TATTGGTGAC
201 CCAGAAAGAT GGAGAGTGGT GGACAGGAAG TATTGGAGAT
241 AGAAGTGGAA TTTTCCATC AACTATGTC AAACCAAAGG
281 ATCAAGAGAG TTTTGGGAGT GCTAGCAAGT CTGGAGCATC
321 AAATAAAAAA CCTGAGATTG CTCAGGTAAC TTCAGCATAT
361 GTTGCTTCTG GTTCTGAACA ACTTAGCCTT GCACCAGGAC
401 AGTTAATATT AATTCTAAAG AAAAATACAA GTGGGTGGTG
441 GCAAGGAGAG TTACAGGCCA GAGGAAAAAA GCGACAGAAA
481 GGATGGTTTC CTGCCAGTCA TGTTAACTT TTGGGTCCAA
521 GCAGTGAAAG AGCCACACCT GCCTTTCATC CTGTATGTCA
561 GGTGATTGCT ATGTATGACT ATGCAGCAAA TAATGAAGAT
601 GAGCTCAGTT TCTCCAAGGG ACAACTCATT AATGTTATGA
641 ACAAAGATGA TCCTGATTGG TGGCAAGGAG AGATCAACGG
681 GGTGACTGGT CTCTTTCCTT CAACTACGT TAAGATGACG
721 ACAGACTCAG ATCCAAGTCA ACAGTGA (SEQ ID NO:39)

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FIG. 52

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1 EFAAASKII PGSEVKREEP EALYAAVNKK PTSAAYSVGE  
41 EYIALYPYSS VEPGDLTFTE GEEILVTQKD GEWWTGSIGD  
81 RSGIFPSNYV KPKDQESFGS ASKSGASNKK PEIAQVTSAY  
121 VASGSEQLSL APGQLILILK KNTSGWWQGE LQARGKKRQK  
161 GWFPASHVKL LGPSSERATP AFHPVCQVIA MYDYAANNED  
201 ELSFSKGQLI NVMNKDDPDW WQGEINGVTG LFPSNYVKMT  
241 TSDPSQQ (SEQ ID NO:40)

FIG. 53

HSLHLHRHQGRKERARYDLEAAQDNELTFKAGEIMTVLDDSDPNWWKGETHQGIGLFPSN 60  
FVTADLTAEPETKTEKTVQFSDDVQVETIEPEPEPAFIDEDKMDQLLOMLQSTDPSSD 120  
QPDLPPELLHLEAMCHQMGPLIDEKLEDIDRKHSELSENVKVMEALSLYTKLMNEDPMYS 180  
MYAKLQNPYYMQSSGVSGSQVYAGPPPSGAYLVAGNAQMSHLQSYSLPPEQLSSLSQAV 240  
VPPSANPALPSQQTQAAYPNRSPGDLMPGDSECRGSAEDSQMRISPPYFPTGQQA 296  
(SEQ ID NO:190)

FIG. 55

IRGRVDQGEWPLPGRGTPGPSGLCVPEDQCRVRDLKGWLSFWAKAEKEE 50  
ENRRLEEKRWAEAAQRQLEQERRERELREAAARREORYQEQGGEASPOSRT 100  
WEQQQEVVSRNRNEQESAVHPREIFKOKERAMSTTSISSPQPGKLRSPFL 150  
QKQLTQPETHFGREPAAAI SRPRADLPAEEPAPSTPPCLVQAEAAVYEE 200  
PPEQETFYEQPPLVQQQGAGSEHIDHHIQGQGLSGQGLCARALYDYQAAD 250  
DTEISFDPENLITGIEVIDEGWWRGYGPDPGHFGMFANYVELIDEAEGTS 300  
CPSPLRHGFLIAGRGGLGVDIOHSSRNRTPSEDEASGLPPAWQTQPVTN 350  
AAMAW 355 (SEQ ID NO:192)

FIG. 57

GRVDIERKRELEMQKKLEDEAARKAKOGKENLWKENLRKEEEEKQKRLQEEKTOEKIQE 60  
EERKAEKQRETASVLVNYRALYPFEARNHDEMFSNSGDI IQVDEKTVGEPGWLYGSFQG 120  
NFGWFPCNYVEKMPSSENEKAVSPKKALLPPTVSLSATSTSSEPLSSNQPASVTDYQNV 180  
FSNLTVNTSWOKKSAFTRTVSPGSVSP IHGQGOVVENLKAQALCSWTAKKDNHLNFSKHD 240  
IITVLEQQENWWFGEVHGGRGWFPKSYVKIIPGSEVKREEPEALYAAVNKKPTSAAYSVG 300  
EEYIALYPYSSVEPGDLTFTEGEEILVTQKDGEWWTGSIGDRSGIFPSNYVKPKDQESFG 360  
SASKSGASNKKPEIAQVTSAYVASGSEQLSLAPGQLILILKKNTSGWWQGE LQARGKKRQ 420  
KGWFPASHVKLLGPSSERATPAFHPVCQVIAMYDYAANNEDLSFSKGQLINVMNKDDPD 480  
WWQGEINGVTGLFPSNYVKMTTSDPSQQ 509 (SEQ ID NO:194)

FIG. 59

CACTCTCTACACTTGCACCGGCATCAAGGACGAAAAGAAC 40  
 GCGCTAGATATGACTTGGAAGCTGCTCAAGACAATGAACT 80  
 TACTTTCAAAGCTGGAGAAATTATGACAGTTCTTGATGAC 120  
 AGTGATCCTAACTGGTGGAAAGGTGAAACCCATCAAGGCA 160  
 TAGGGTTATTTCTTCTAATTTTGTGACTGCAGATCTCAC 200  
 TGCTGAACCAGAAATGATTAACAGAGAAGAAGACGGTA 240  
 CAATTTAGTGATGATGTTTCAGGTAGAGACAATAGAACCAG 280  
 AGCCGGAACCAGCCTTTATTGATGAAGATAAAATGGACCA 320  
 GTTGCTACAGATGCTGCAAAGTACAGACCCAGTGATGAT 360  
 CAGCCAGACCTACCAGAGCTGCTTCATCTTGAAGCAATGT 400  
 GTCACCAGATGGGACCTCTCATTGATGAAAAGCTGGAAGA 440  
 TATTGATAGAAAACATTCAGAACTCTCAGAACTTAATGTG 480  
 AAAGTGATGGAGGCCCTTTCCTTATATACCAAGTTAATGA 520  
 ACGAAGATCCGATGTATTCCATGTATGCAAAGTTACAGAA 560  
 TCAGCCATATTATATGCAGTCATCTGGTGTCTGTTCT 600  
 CAGGTGTATGCAGGGCTCCTCCAAGTGGTGCCTACCTGG 640  
 TTGCAGGGAACGCGCAGATGAGCCACCTCCAGAGCTACAG 680  
 TCTTCCCCCGGAGCAGCTGTCTTCTCTCAGCCAGGCAGTG 720  
 GTCCCACCATCCGCAAACCCAGCCCTTCTAGTCAGCAGA 760  
 CTCAGGCCGCTTACCCAAACCGCTCCCCAGGGGACCTCAT 800  
 GAAGCCCGGTGATTCTGAATGCCGTGGATCTGCCGAGGAT 840  
 TCCCAGATGCGTATTTCTCCTCCGTACTTCCCCACAGGAC 880  
 AGCAGGCTTGAATAGCTGATTGCCTATGCAGGACAACAGG 920  
 CTTGAATAGCTGACTGCCTATGCATTCTCTTTGCTTGCCA 960  
 GTTTTTTGGACATCAAACCTTGACAGATCCAAGATTATTAC 1000  
 TTTGATCTTCCCCACACCCCTCCCACCCCGAGTCTACTA 1040  
 TGGTCCCATCATAGTATTCTGAAAATCAGTGAATGGCCAC 1080  
 TCTACCAGTTATTTCTACCAGTTTTTAGGTTCTAAACCTC 1120  
 AGGCATTCTGGACTCTTCTGTTCATTATCATATTTTGAAG 1160  
 GCATTATCTTCAAATCTATCTAGACTCTGACCCTTTCTC 1200  
 CCATCTCCACCATTACTGCCGTGGCTCTTCTGCTGGTCGG 1240  
 CTCTCTCCTGGTGGATCCGTAATAACCTGCAGTCAGCTAT 1280  
 CCTGGTCCAGAAGGGAACCCCGTTAAACCCTGTTGGAATC 1320  
 TTATCACGCTTCTGCTCCAGAACGAACCCAGTCTGTCTGT 1360  
 CTCCTCAGAGTGTAAGCTACAGTCCTTATTGTGGCCATC 1400  
 AGGTGCTGTGTGTTCTCCAGCCCCCTCCCCACCACCGCAG 1440  
 TCCTGCCGGTGATCTTAGCTGCTCTCCCCTCGGAACCCCT 1480  
 TGCGGCCCCCTCTGCCGCAACAXTCGTGGCCTGCTGTTCC 1520  
 TTGAACATGCTTGGTGTCTCTCCTCAAAGGCTTCTTT 1560  
 CTGTTTACCTGAAATGTACTTGCCTAGGGAAATCTTATCC 1600  
 TGGCTCACTCCGCTTACTTTTTTCCACATCTTTGCTTAAA 1640  
 GTTATTGCCCTTATTGGAGAAGGCACCCCTACCATAAACT 1680  
 AGAAATCCCTTGCCCCCAAGCTGCTCCTTT 1710

(SEQ ID NO:189)

FIG. 54



GAATTCGCGGCCGCGTCGACCAAGGAGAGTGGCCGCTTCC 40  
 AGGACGTGGGACCCAGGCCCCAGTGGGCTCTGTGTACCA 80  
 GAAGACCAATGCCGTGTCAGAGATTTAAAGGGTTGGTTAG 120  
 ACAGCTTCTGGGCCAAAGCAGAGAAGGAGGAGGAGAACCG 160  
 TCGGCTGGAGGAAAAGCGGTGGGCCGAGGAGGCACAGCGG 200  
 CAGCTGGAGCAGGAGCGCCGGGAGCGTGAGCTGCGTGAGG 240  
 CTGCACGCCGGGAGCAGCGCTATCAGGAGCAGGGTGGCGA 280  
 GGCCAGCCCCAGAGCAGGACGTGGGAGCAGCAGCAAGAA 320  
 GTGGTTTCAAGGAACCGAAATGAGCAGGAGTCTGCCGTGC 360  
 ACCCGAGGGAGATTTTCAAGCAGAAGGAGAGGGCCATGTC 400  
 CACCACCTCCATCTCCAGTCCTCAGCCTGGCAAGCTGAGG 440  
 AGCCCCTTCTGCAGAAGCAGCTCACCCAACCAGAGACCC 480  
 ACTTTGGCAGAGAGCCAGCTGCTGCCATCTCAAGGCCCAG 520  
 GGCAGATCTCCCTGCTGAGGAGCCGGCGCCAGCACTCCT 560  
 CCATGTCTGGTGCAGGCAGAAGAGGAGGCTGTGTATGAGG 600  
 AACCTCCAGAGCAGGAGACCTTCTACGAGCAGCCCCACT 640  
 GGTGCAGCAGCAAGGTGCTGGCTCTGAGCACATTGACCAC 680  
 CACATTAGGGCCAGGGGCTCAGTGGGCAAGGGCTCTGTG 720  
 CCCGTGCCCTGTACGACTACCAGGCAGCCGACGACACAGA 760  
 GATCTCCTTTGACCCCGAGAACCTCATCACGGGCATCGAG 800  
 GTGATCGACGAAGGCTGGTGGCGTGGCTATGGGCCGGATG 840  
 GCCATTTTGGCATGTTCCCTGCCAATTACGTGGAGCTCAT 880  
 TGATGAGGCTGAGGGCACATCTTGCCCTTCCCCTCTCAGA 920  
 CATGGCTTCCTTATTGCTGGAAGAGGAGGCCTGGGAGTTG 960  
 ACATTCAGCACTCTTCCAGGAATAGGACCCCCAGTGAGGA 1000  
 TGAGGCCTCAGGGCTCCCTCCGGCTTGGCAGACTCAGCCT 1040  
 GTCACCCCAAATGCAGCAATGGCCTGGTGATTCCACACA 1080  
 TCCTTCCTGCATCCCCGACCCTCCCAGACAGCTTGGCTC 1120  
 TTGCCCTGACAGGATACTGAGCCAAGCCCTGCCTGTGGC 1160  
 CAAGCCCTGAGTGGCCACTGCCAAGCTGCGGGGAAGGGTC 1200  
 CTGAGCAGGGGCATCTGGGAGGCTCTGGCTGCCTTCTGCA 1240  
 TTTATTTGCCTTTTTTCTTTTTCTTTGCTTCTAAGGGGT 1280  
 GGTGGCCACCACTGTTTAGAATGACCCTTGGGAACAGTGA 1320  
 ACGTAGAGAATTGTTTTAGCAGAGTTTGTGACCAAAGTC 1360  
 AGAGTGGATCATGGTGGTTTGGCAGCAGGGAATTTGTCTT 1400  
 GTTGGAGCCTGCTCTGTGCTCCCCACTCCATTTCTCTGTC 1440  
 CCTCTGCCTGGGCTATGGGAAGTGGGGATGCAGATGGCCA 1480  
 AGCTCCCACCCTGGGTATTCAAAAACGGCAGACACAACAT 1520  
 GTTCCTCCACGCGGCTCACTCGATGCCTGCAGGCCCCAGT 1560  
 GTGTGCCTCAACTGATTCTGACTTCAGGAAAAGTAACACA 1600  
 GAGTGGCCTTGGCCTGTTGTCTTCCCCTATTTTCTGTCCC 1640  
 AGCTCATCCGTGGTCAAGCGCCCGCAATTCCAGCTGAG 1680  
 CGGCCGC 1687 (SEQ ID NO:191)

FIG. 56

GCGGCCGCGTCGACATTGAAAGGAAAAGATTAGAACTAAT	40
GCAGAAAAAGAACTAGAAAGATGAGGCTGCAAGGAAAGCA	80
AAGCAAGGAAAAGAAAACCTTATGGAAAGAAAATCTTAGAA	120
AGGAGGAAGAAGAAAAACAAAAGCGACTCCAGGAAGAAAA	160
AACACAAGAAAAAATTCAAGAAGAGGAACGGAAAGCTGAG	200
GAGAAACAACGTGAGACAGCTAGTGTTTTGGTGAATTATA	240
GAGCATTATACCCCTTTGAAGCAAGGAACCATGATGAGAT	280
GAGTTTTAATTCTGGAGATATAATTCAGGTTGATGAAAAA	320
ACCGTAGGAGAACCTGGTTGGCTTTATGGTAGTTTTCAAG	360
GAAATTTTGGCTGGTTTCCATGCAATTATGTAGAAAAAAT	400
GCCATCAAGTGAAAATGAAAAAGCTGTATCTCCAAAGAAG	440
GCCTTACTTCCTCCTACAGTTTCTTTATCTGCTACCTCAA	480
CTTCCTCTGAACCACTTTCTTCAAATCAACCAGCATCAGT	520
GACTGATTATCAAAATGTATCTTTTTCAAACCTAACTGTA	560
AATACATCATGGCAGAAAAAATCAGCCTTCACTCGAACTG	600
TGTCCCCTGGATCTGTATCACCTATTCATGGACAGGGACA	640
AGTGGTAGAAAACTTAAAGCACAGGCCCTTTGTTCTCGG	680
ACTGCAAAGAAAGATAACCACTTGAACCTCTCAAAACATG	720
ACATTATTACTGTCTTGGAGCAGCAAGAAAATTGGTGGTT	760
TGGGGAGGTGCATGGAGGAAGAGGATGGTTTCCCAAATCT	800
TATGTCAAGATCATTCCTGGGAGTGAAGTAAACGGGAAG	840
AACCAGAAGCTTTGTATGCAGCTGTAAATAAGAAACCTAC	880
CTCGGCAGCCTATTCAAGTGGAGAAGAATATATTGCACTT	920
TATCCATATTCAAGTGTGGAACCTGGAGATTTGACTTTCA	960
CAGAAGGTGAAGAAATATTGGTGACCCAGAAAGATGGAGA	1000
GTGGTGGACAGGAAGTATTGGAGATAGAAGTGAATTTTTT	1040
CCATCAAACCTATGTCAAACCAAGGATCAAGAGAGTTTTG	1080
GGAGTGCTAGCAAGTCTGGAGCATCAAATAAAAAACCTGA	1120
GATTGCTCAGGTAACCTCAGCATATGTTGCTTCTGGTTCT	1160
GAACAACCTTAGCCTTGCACCAGGACAGTTAATATTAATTC	1200
TAAAGAAAAATACAAGTGGGTGGTGGCAAGGAGAGTTACA	1240
GGCCAGAGGAAAAAAGCGACAGAAAGGATGGTTTCCTGCC	1280
AGTCATGTTAACTTTTGGGTCCAAGTAGTGAAAGAGCCA	1320
CACCTGCCTTTCATCCTGTATGTCAGGTGATTGCTATGTA	1360
TGACTATGCAGCAAATAATGAAGATGAGCTCAGTTTCTCC	1400
AAGGGACAACCTATTAATGTTATGAACAAAGATGATCCTG	1440
ATTGGTGGCAAGGAGAGATCAACGGGGTGAAGTGGTCTCTT	1480
TCCTTCAAACCTACGTTAAGATGACGACAGACTCAGATCCA	1520
AGTCAACAGTGACCCAATGTTGTCTTCCAGTTGTGAAAGC	1560
ACCCAGAGACCCACTATCCAAGTTTCACTCTAGCGTGGA	1600
GGCAGGGCAGGCAGCCCTGATCAAATATCTGCTACACAAT	1640
TCGTTTACTTCGTTTGAATGTTAGAGCCACTTGTGATTAT	1680
TTTTTTGTGTTTCTAACTTACAGTTTAAATTTATTTGTAA	1720

FIG. 58A

AAAGTTAAAGGATAGTGGGTCTTTGTGTGGCTTTCCCTGC 1760  
TGTTCACTCTGGCATCTTTAGCATTTTTCTTCTTTTTTAA 1800  
TTTGATAATTGTAGGTCATTAGCATGCATATTGAGTTTGC 1840  
CGTTATGTGGTGGGAGTTCAAACACACAAAGACCCACTAT 1880  
TTGCACAACTATTCTTACTGGTTTGGAATAGGCTGCCAT 1920  
GCTTTTTTAATGTTATTGCAACATGTGTATTCATTTACAG 1960  
AATTCAGATAAAATTTGCTTATGTTCTGCTATTATGTTTG 2000  
ATCTAATCCTAATCACAGTGAGCTCTTAATTAGCTCAATA 2040  
TGTGGTTTGCCCTCAAGTGTGCACTGTTTATTACTTTTGA 2080  
ATATGCCACTATGAGTACTGACATTTAGATATGTTTAAAG 2120  
GCCAAGAACTGGAAACAGCCATGCCCTGTTTTCTGTGTAT 2160  
TTGGGATGGGAATAACAACATTTTGGGGGAGCTTTTTTAA 2200  
ATCTCAGAGAAGAGGAAAGTGGCCTGCTCTGGCAGGTATG 2240  
TGCAGTGTTTCATTTGTTCCAGTCCCAAGAATGAGCACTG 2280  
TCCTATGGTAGTTTCGCTTAGGATCTTTATGTGCTCTGGGC 2320  
TAATGAAGGTACTGCATCATGTGCTGCAGCGTGTGTATTC 2360  
TTTTTCGATGACCTATAAAGGGATTATTTTTGAGGAATGA 2400  
AAGGCTCCCATCATTGACTGTGAGATGGGAAAAACCTTTC 2440  
CTAGCTTAGAGCATTTATATCTTAATCCATTTTAAAGTCA 2480  
GAGTTCATTGTTACCTGTTTTAATCAGGTGACTACATGTC 2520  
CCAGTATACAAAGGGGCACTGGTTGACATTCTTCTTAATG 2560  
TATTTAGTAAATATCATAAGAAATCCTTTAAGAGTTTAAA 2600  
TGTCCCCAAAACAGACATGCGGGCTCTAGTCAAGAATGAA 2640  
TTAGAGTGAAGGAAAGCTGTGTAACACCTGGCATTCTCT 2680  
GTGTTTCATGGAGCTTCTTTGAGGCTCTAAGATTGATTTTA 2720  
CCATCAGACTTCTCTAATACCTGTTCTTCAACCATATTGG 2760  
CTACTTTGACATAAGAATTTACTTCTTTTCTGGAATGGA 2800  
AAACACTTTAAAAAATAATAACAAACATTATTATAAACTA 2840  
ATATATGTGAGAGGTGACGCGGCCGCGAATTC 2873

(SEQ ID NO:193)

FIG. 58B

GAATTCGTCGACCCACGCGTCCGAAATATAACTGAAGTTGGGGCACCTAC 50  
 TGAAGAAGAGGAAGAAAGTGAAAGTGAAGATAGTGAAGACAGTGGTGGGG 100  
 AGGAAGAAGATGCAGAGGAGGAAGAGGAAGAGAAAGAGGAAAAATGAATCT 150  
 CACAAATGGTCAACCGGTGAAGAATACATCGCTGTTGGAGATTTTACTGC 200  
 TCAGCAAGTTGGAGATCTTACATTTAAGAAAGGGGAAATTCTCCTTGTA 250  
 TTGAAAAAAACCTGATGGTTGGTGGATAGCTAAGGATGCCAAAGGAAAT 300  
 GAAGGTCTTGTTCCAGAACCTACCTAGAGCCTTATAGTGAAGAAGAAGA 350  
 AGGCCAAGAGTCAAGTGAAGAGGGCAGTGAAGAAGATGTAGAGGCGGTGG 400  
 ATGAAACAGCAGATGGAGCAGAAGTTAAGCAAAGAAGTATCCCCACTGG 450  
 AGTGTCTGTTAGAAAGCGATTTAGAGGCGGGCATCTTCTGTCTTGTTAA 500  
 TCATGTCTCGTTTTGCTACCTAATAGTTCTGATCCGTCCTAA 543  
 (SEQ ID NO:196)

FIG. 60

GAATTCGGCGGACTTCGCGGCCGCGTCGACGAAGAAACCT 40  
 GAAGGACACACTAGGCCTCGGCAAGACGCGCAGGAAGACC 80  
 AGCGCGCGGGATGCGTCCCCACGCCCAGCACGGACGCCG 120  
 AGTACCCCGCCAATGGCAGCGCGCCGACCGCATCTACGA 160  
 CCTCAACATCCCGGCCTTCGTCAAGTTCGCCTATGTGGCC 200  
 GAGCGGGAGGATGAGTTGTCCCTGGTGAAGGGTTCGCGCG 240  
 TCACCGTCATGGAGAAGTGCAGCGACGGTTGGTGGCGGGG 280  
 CAGCTACAACGGGCAGATCGGCTGGTTCCCCTCCAACCTAC 320  
 GTCTTGAGGAGGTGGACGAGGCGGTTGCGGAGTCCCCAA 360  
 GCTTCCTGAGCCTGCGCAAGGGCGCCTCGCTGAGCAATGG 400  
 CCAGGGCTCCCGCGTGCTGCATGTGGTCCAGACGCTGTAC 440  
 CCCTTCAGCTCAGTCACCGAGGAGGAGCTCAACTTCGAGA 480  
 AGGGGGAGACCATGGAGGTGATTGAGAAGCCGGAGAACGA 520  
 CCCCAGTGGTGGAAATGCAAAAATGCCCGGGGCCAGGTG 560  
 GGCCTCGTCCCCAAAACTACGTGGTGGTCTCAGTGACG 600  
 GGCCTGCCCTGCACCCTGCGCACGCCCCACAGATAAGCTA 640  
 CACCGGGCCCTCGTCCAGCGGGCGCTTCGCGGGCAGAGAG 680  
 TGGTACTACGGGAACGTGACGCGGCACCAGGCCGAGTGCG 720  
 CCCTCAACGAGCGGGGCGTGGAGGGCGACTTCCTCATTAG 760  
 GGACAGCGAGTCCTCGCCCAGCGACTTCTCCGTGTCCCTT 800  
 AAAGCGTCAGGGAAGAACAACACTTCAAGGTGCAGCTCG 840  
 TGGACAATGTCTACTGCATTGGGCAGCGGCGCTTCCACAC 880  
 CATGGACGAGCTGGTGGAACTACAAAAAGGCGCCCATC 920  
 TTCACCAGCGAGCACGGGGAGAAGCTCTACCTCGTCAGGG 960  
 CCCTGCAGTGA 971 (SEQ ID NO:197)

FIG. 62

GAATTCGTCGACCCACGGTCCGAAATATAACTGAAGTTGGGGCACCTACTGAAGAAGAGGAAGAAAGTG	70
+++++	
E F V D P R V R N I T E V G A P T E E E E E S	23
+++++	
AAAGTAAGATAGTGAAGACAGTGGTGGGGAGCAAGAAGATGCAGAGGAGGAAGAGAAAGAGGA	140
+++++	
E S E D S E D S G G E E E D A E E E E E E K E E	47
+++++	
AAATGAATCTCACAAATGGTCAACCGGTGAAGAATACATCGCTGTTGGAGATTTTACTGCTCAGCAAGTT	210
+++++	
N E S H K W S T G E E Y I A V [G D F T A Q Q V	70
+++++	
GGAGATCTTACATTTAAGAAAGGGGAAATTCCTTGTAATTGAAAAAACCTGATGGTTGGTGGATAG	280
+++++	
G D L T F K K G E I L L V I E K K P D G W W I	93
+++++	
CTAAGGATGCCAAAGGAAATGAAGGTCTTGTTCCAGAACCTACCTAGAGCCTTATAGTGAAGAAGAAGA	350
+++++	
A K D A K G N E G L V P R T Y] L E P Y S E E E E	117
+++++	
AGGCCAAGAGTCAAGTGAAGAGGGCAGTGAAGAAGATGTAGAGCGGTGGATGAAACAGCAGATGGAGCA	420
+++++	
G Q E S S E E G S E E D V E A V D E T A D G A	140
+++++	
GAAGTTAAGCAAAGAACTGATCCCCACTGGAGTGCTGTTTCAGAAAGCGATTTTCAGAGCGGGCATCTTTT	490
+++++	
E V K Q R T D P H W S A V Q K A I S E A G I F	163
+++++	

FIG.61A

---

GTCTTGTTAATCATGTCTCGTTTTGCTACCTAATAGTTCTGATCCGTCCTAA  
+++++  
C L V N H V S F C Y L I V L I R P 180  
+++++

(SEQ ID NO:196)

FIG.61B

GAATTCGGCGGACTTCGCGGCCGCGTCGACGAAGAAACCTGAAGGACACACTAGGCCTCGGCAAGACGCG	70
I R R T S R P R R R R N L K D T L G L G K T R	23
CAGGAAGACCAGCGCGCGGATGCGTCCCCACGCCACGACGCGGAGTACCCCGCCAATGGCAGC	140
R K T S A R D A S P T P S T D A E Y P A N G S	46
GGCGCCGACCGCATCTACGACCTCAACATCCCGGCCTTCGTCAAGTTCGCCTATGTGGCCGAGCGGGAGG	210
G A D R I Y D L N I P A F V K [F A Y V A E R E	69
ATGAGTTGTCCCTGGTGAAGGGTCCGCGCTCACCGTCATGGAGAAGTGCAGCGACGGTTGGTGGCGGGG	280
D E L S L V K G S R V T V M E K C S D G W W R G	93
CAGCTACAACGGGCAGATCGGCTGGTTCCCTCCAACCTACGTCTTGGAGGAGGTGGACGAGGCGGTTGCG	350
S Y N G Q I G W F P S N Y] V L E E V D E A V A	116
GAGTCCCCAAGCTTCCTGAGCCTGCGCAAGGGCGCCTCGCTRGAGCAATGCCAGGGCTCCCGCGTGCTGC	420
E S P S F L S L R K G A S L S N G Q G S R V L	139
ATGTGGTCCAGACGCTGTACCCCTTCAGCTCAGTCACCGAGGAGGAGCTCAACTTCGAGAAGGGGGAGCAC	490
H V V Q T L [Y P F S S V T E E E L N F E K G E T	163

FIG.63A

```

CATGGAGGTGATTGAGAAGCCGGAGAACGACCCCGAGTGGTGGAAATGCAAAATGCCCGGGCCAGGTG
|-----| 560
  M E V I E K P E N D P E W W K C K N A R G Q V 186
|-----|
GGCCTCGTCCCCAAAACTACGTGGTGGTCCTCAGTGACGGGCTGCCCTGCACCCTGCGCACGCCCCAC
|-----| 630
  G L V P K N Y] V V V L S D G P A L H P A H A P 209
|-----|
AGATAAGCTACACCGGGCCCTCGTCCAGCGGGCGCTTCGCGGGCAGAGAGTGGTACTACGGGAACGTGAC
|-----| 700
  Q I S Y T G P S S S G R F A G R E W Y Y G N V T 233
|-----|
GCGGCACCAGGCCGAGTGGCCCTCAACGAGCGGGCGTGGAGGGCGACTTCCTCATTAGGGACAGCGAG
|-----| 770
  R H Q A E C A L N E R G V E G D F L I R D S E 256
|-----|
TCCTCGCCCAGCGACTTCTCCGTGTCCCTTAAAGCGTCAGGAAGAACAACACTTCAAGGTGCAGCTCG
|-----| 840
  S S P S D F S V S L K A S G K N K H F K V Q L 279
|-----|
TGGACAATGTCTACTGCATTGGGCAGCGGCGCTTCACACCATGGAGGAGCTGGTGGAACTACAAAAA
|-----| 910
  V D N V Y C I G Q R R F M T M D E L V E H Y K K 303
|-----|
GGCGCCCATCTTCACCAGCGAGCACGGGGAGAAGCTCTACCTCGTCAGGGCCCTGCAGTGACGGCGCCCC
|-----|
                                STOP 980
  A P I F T S E H G E K L Y L V R A L Q /322
|-----|

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(SEQ ID NO:198)

FIG.63B



GAATTCGCGGACTTCGCGGCCGCGTCGACACCAGTGCAGG 40  
TTTTGGAATATGGAGAAGCTATTGCTAAGTTTAACTTTAA 80  
TGGTGATACACAAGTAGAAATGTCCTTCAGAAAGGGTGAG 120  
AGGATCACACTGCTCCGGCAGGTAGATGAGAACTGGTACG 160  
AAGGGAGGATCCCGGGGACATCCCGACAAGGCATCTTCCC 200  
CATCACCTACGTGGATGTGATCAAGCGACCACTGGTGAAA 240  
AACCCTGTGGATTACATGGACCTGCCTTTCTCCTCCTCCC 280  
CAAGTCGCAGTGCCACTGCAAGCCCACAGCAACCTCAAGC 320  
CCAGCAGCGAAGAGTCACCCCGACAGGAGTCAAACCTCA 360  
CAAGATTTATTTAGCTATCAAGCATTATATAGCTATATAC 400  
CACAGAATGATGATGAGTTGGAACCTCCGCGATGGAGATAT 440  
CGTTGATGTCATGGAAAAATGTGACGATGGATGGTTTGTT 480  
GGTACTTCAAGAAGGACAAAGCAGTTTGGTACTTTTCCAG 520  
GCAACTATGTAAACCTTTGTATCTATAA (SEQ ID NO:199)

FIG. 64

GAATTCGCGGACTTCGCGGCCGCTCGACACCAGTGCAGGTTTTGGAATATGGAGAAGCTATTGCTAAGT  
 ++++++ 70  
 CTTAAGCGCCTGAAGCGCCGGCGCAGCTGTGGTCACGTCCAAAACCTTATACCTCTTCGATAACGATTCA  
 ++++++  
 ORF  
 (E) F A D F A A A S T P V Q V L E Y G E A I A K 23  
 ++++++  
 TTAACITTAATGGTGATACACAAGTAGAAATGTCCTTCAGAAAGGGTGAGAGGATCACACTGCTCCGGCA  
 ++++++ 140  
 AATTGAAATTACCACTATGTGTTTCATCTTTACAGGAAGTCTTTCCCACTCTCCTAGTGTGACGAGGCCGT  
 ++++++  
 F N F N G D T Q V E M S F R K G E R I T L L R Q 47  
 ++++++  
 GGTAGATGAGAACTGGTACGAAGGGAGGATCCCGGGGACATCCCGACAAGGCATCTTCCCATCACCTAC  
 ++++++ 210  
 XXATCTACTCTTGACCATGCTTCCCTCCTAGGGCCCTGTAGGGCTGTTCCGTAGAAGGGGTAGTGGATG  
 ++++++  
 V D E N W Y E G R I P G T S R Q G I F P I T Y 70  
 ++++++  
 GTGGATGTGATCAAGCGACCACTGGTGAAAACCCCTGTGGATTACATGGACCTGCCTTTCTCCTCCTCCC  
 ++++++ 280  
 CACCTACACTAGTTGCTGGTGACCACTTTTTGGGACACCTAATGTACCTGGACGGAAGAGGAGGAGG  
 ++++++  
 V D V I K R P L V K N P V D Y M D L P F S S S 93  
 ++++++  
 CAAGTCGCAGTCCCACTGCAAGCCCACAGCAACCTCAAGCCCAGCAGCGAAGAGTACCCCCGACAGGAG  
 ++++++  
 GTTCACCGTCACGGTGACGTTGGGTGTCGTTGGAGTTCGGGTCGTCGCTTCTCAGTGGGGGCTGTCCTC 350  
 ++++++  
 P S R S A T A S P Q Q P Q A Q Q R R V T P Q R S 117  
 ++++++

FIG.65A

TCAAACCTCACAAGATTTATTTAGCTATCAAGCATTATATAGCTATATACCACAGAATGATGATGAGTTG 420  
AGTTTGGAGTGTTCTAAATAAATCGATAGTTCGTAATATATCGATATATGGTGTCTTACTACTACTCAAC  
SH3  
Q T S Q D L F S Y Q A L [Y S Y] I P Q N D [D E L] 140  
GAACTCCGGATGGAGATATCGTTGATGTCATGAAAAATGTGACGATGGATGGTTTGTGGTACTTCAA 490  
CTTGAGGCGCTACCTCTATAGCAACTACAGTACCTTTTTACACTGCTACCTACCAAACAACCATGAAGTT  
F  
E L R D G D I V D V M E K C D D G [W F] V G T S 163  
GAAGGACAAAGCAGTTTGGTACTTTCCAGGCAACTATGTAAACCTTTGTATCTATAAGAAGACTGAAA 560  
CTTCCTGTTTCGTCAAACCATGAAAAGGTCCGTTGATACATTTTGGAAACATAGATATTCTTCTGACTTT  
STOP  
R R T K Q F G T F [R G N Y] V K P L Y L ( ) 181  
(SEQ ID NO:200)

FIG.65B

AATCAAGCGCGGGTCTTTAGGATTTGCAGCTCCAGGAAGCGAGATGTCGAAGCGCCACCCAAACCA  
 +-----+ 70  
 N S S A G S L G F A A P G S E M S K P P P K P  
 +-----+  
 GTCAAACCAGGGCAAGTTAAAGTCTTCAGAGCCCTGTATACGTTTGAACCCAGAACTCCAGATGAATTAT  
 +-----+ 140  
 V K P G Q V K V F R A L Y T F E P R T P D E L  
 +-----+  
 ACTTTGAGGAAGGTGATATTATCTACATTACTGACATGAGCGATACCAATTGGTGGAAAGGCACCTCCAA  
 +-----+ 210  
 Y F E E G D I I Y I T D M S D T N W W K G T S K  
 +-----+  
 AGGCAGGACTGGACTAATTCCAAGCAACTATGTGGCTGAGCAGGCAGAATCCATTGACAATCCATTGCAT  
 +-----+ 280  
 G R T G L I P S N Y V A E Q A E S I D N P L H  
 +-----+  
 GAAGCAGCAAAAAGAGGCAACTTGAGCTGGTTGAGAGAGTGTTTGGACAACAGAGTGGGTGTTAATGGCT  
 +-----+ 350  
 E A A K R G N L S W L R E C L D N R V G V N G  
 +-----+  
 TAGACAAAGCTGGAAGCACTGCCTTATACTGGGCTTGCCACGGGGCCACAAAGATATAGTGGAAATGCT  
 +-----+ 420  
 L D K A G S T A L Y W A C H G G H K D I V E M L  
 +-----+  
 ATTTACTCAACCAAATATTGAACTGAACCAGCAGAACAAGTTGGGAGATACAGCTTTGCATGCTGCTGCC  
 +-----+ 490  
 F T Q P N I E L N Q D N K L G D T A L H A A A  
 +-----+

FIG.66A

TGGAAGGGTTATGCAGATATCGTCCAGTTGCTTCTGCCAAAAGGTGCTAGAACAGACTTAAGAAACATTG 560  
W K G Y A D I V Q L L L A K G A R T D L R N I  
AGAAGAAGCTGGCCTTCGACATGGCTACCAATGCTGCCTGTGCATCTCTCCTGAAAAAGAAACAGGGAAC 630  
E K K L A F D M A T N A A C A S L L K K K Q G T  
AGATGCAGTTCGAACATTAAGCAATGCCGAGGACTATCTCGATGATGAAGACTCAGATTAA  
D A V R T L S N A E D Y L D D E D S D <sup>STOP</sup>  
^

(SEQ ID NO:221)

FIG.66B